



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 194666**

**TO: Minh-Tam Davis**  
**Location: 3a24 / 3c18**  
**Thursday, July 06, 2006**  
**Art Unit: 1642**  
**Phone: 571-272-0830**  
**Serial Number: 09 / 403440**

**From: Jan Delaval**  
**Location: Biotech-Chem Library**  
**Remsen 1a51**  
**Phone: 571-272-2504**

**jan.delaval@uspto.gov**

### **Search Notes**

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73622

194666

M9

**STIC-Biotech/ChemLib**

**From:** Chan, Christina  
**Sent:** Wednesday, July 05, 2006 9:56 AM  
**To:** Davis, Minh-Tam; STIC-Biotech/ChemLib  
**Subject:** RE: Rush search request for 09/403440

Please ~~rush~~ Thanks Chris

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

-----Original Message-----

**From:** Davis, Minh-Tam  
**Sent:** Monday, July 03, 2006 11:37 AM  
**To:** Chan, Christina  
**Subject:** Rush search request for 09/403440

Please search in commercial database, issued patent files and PGUB:  
The peptide SEQ ID NO:2, with and without size limitation for the sequences in the database to the size of SEQ ID NO:2.

Thank you.  
MINH TAM DAVIS  
ART UNIT 1642, ROOM 3A24, MB 3C18  
272-0830

\*\*\*\*\*

Searcher: Chen  
Searcher Phone: 22504  
Date Searcher Picked up: 7/11/06  
Date completed: 7/16/06  
Searcher Prep Time: 10  
Online Time: 15

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# 1  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: ✓  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 22:41:06 ; Search time 39 Seconds  
(without alignments)  
46.875 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSIDLWKLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	94.3	391	2	JC6193 tumor suppressor p
2	99	94.3	393	1	DNH053 cellular tumor ant
3	99	94.3	393	1	S06594 cellular tumor ant
4	94	89.5	386	1	S51648 cellular tumor ant
5	86	81.9	393	2	JC6176 tumor suppressor p
6	86	81.9	396	1	JH0633 cellular tumor ant
7	81	77.1	363	1	A29376 cellular tumor ant
8	74	70.5	381	2	S38824 cellular tumor ant
9	74	70.5	390	1	DNM553 cellular tumor ant
10	72	68.6	391	1	S02192 cellular tumor ant
11	60	57.1	396	1	JH0631 cellular tumor ant
12	51.5	49.0	1009	2	S28857 glutamate receptor
13	51.5	49.0	1009	2	JH0266 glutamate receptor
14	50	47.6	230	2	C64396 pectorin-2 methyl
15	50	47.6	367	2	G68715 racemase [imported
16	50	47.6	447	2	E96672 Similar to Flavono
17	48	45.7	119	2	C49921 cysterol-binding
18	48	45.7	308	2	AD3262 methyltransferase
19	48	45.7	1004	2	B25039 outer cell wall pr
20	47	44.8	157	1	VCTMPV coat protein - pep
21	47	44.8	469	2	G84779 hypothetical prote
22	47	44.8	487	2	D83027 hypothetical prote
23	47	44.8	489	2	T41241 cytoskeleton-binding
24	47	44.8	956	2	G70327 isolucine-tRNA i
25	46.5	44.3	250	2	T01604 hypothetical prote
26	46.5	44.3	485	2	C75460 hypothetical prote
27	46	43.8	274	2	S74792 hypothetical prote
28	46	43.8	293	1	D69300 4-hydroxybenzoate
29	45.5	43.3	250	2	T49221 hypothetical prote

30	45	42.9	367	2	E96796 hypothetical prote
31	45	42.9	405	2	AD2194 hypothetical prote
32	45	42.9	837	2	I57557 DNA-Binding Protei
33	44.5	42.4	211	2	B95064 conserved hypothet
34	44.5	42.4	211	2	D97931 conserved hypothet
35	44	41.9	113	1	P3WLB4 I3 protein - bovin
36	44	41.9	114	2	S03072 hypothetical prote
37	44	41.9	124	2	A82749 hypothetical prote
38	44	41.9	209	2	S61204 NEF protein - simi
39	44	41.9	211	1	ASLQMS nef protein - simi
40	44	41.9	238	2	S61205 NEF protein - simi
41	44	41.9	239	2	S61206 NEF protein - simi
42	44	41.9	239	2	S54852 nef protein - simi
43	44	41.9	244	2	S61208 NEF protein - simi
44	44	41.9	246	2	S54853 nef protein - simi
45	44	41.9	250	2	S54849 nef protein - simi

#### ALIGNMENTS

##### RESULT 1

JC6193 tumor suppressor p53 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 11-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 09-Jul-2004

C:Accession: JC6193

R:Le Goas, F.; May, P.; Ronco, P.; de Fromental, C.C.

Gene 185, 169-173, 1997

A>Title: cDNA cloning and immunological characterization of rabbit p53.

A:Reference number: JC6193; PMID:97208869; PMID:9055811

A:Accession: JC6193

A:Molecule type: mRNA

A:Residues: 1-391 <LEA>

A:Cross-references: UNIPROT:Q95330; UNIPARC:UPI0000131047; EMBL:X90592; NID:g1532043; P

C:Genetics:

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: tumor

Query Match 94.3%; Score 99; DB 2; Length 391;

Best Local Similarity 100.0%; Pred. No. 3.2e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSIDLWKLPEN 18

Db 12 PPLSQETFSIDLWKLPEN 29

|||||

##### RESULT 2

DNH053 cellular tumor antigen p53 [validated] - human

N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppress

C:Species: Homo sapiens (man)

C>Date: 05-Oct-1988 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A25224; A43073; J0436; S40773; S42669; A28373; A55060; A25397; B25397; S4

4905; I58354; I78850; I52681; S60153

R:Lamb, P.; Crawford, L.

Mol. Cell. Biol. 6, 1379-1385, 1986

A>Title: Characterization of the human p53 gene.

A:Reference number: A25224; PMID:87064416; PMID:2946935

A:Accession: A25224

A:Molecule type: DNA

A:Residues: 1-393 <LMA>

A:Cross-references: UNIPROT:P04637; UNIPARC:UPI000006F8F0; EMBL:X01405; GB:M13121; GB:N

R:Buchan, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.

Gene 70, 245-252, 1988

A>Title: A variation in the structure of the protein-coding region of the human p53 gen

A:Reference number: J0436; PMID:89108008; PMID:2905688

A:Accession: A43073

A:Molecule type: DNA

A:Residues: 1-393 <BUC1>

A:Cross-references: UNIPARC:UPI000006F8F0; EMBL:M2898; NID:g189474

A>Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro allele

A:Accession: J0436

A:Molecule type: DNA

A:Residues: 1-71, 'P', 73-393 <BUCA>

A:Cross-references: UNIPARC:UPI000002ED67; EMBL:M22898; NID:g169474; PIDN:AAA59988.1; PI

A>Note: this 72-Pro allele was found in both normal and malignant cell lines

R:Chunakov, P.M.; Almazov, V.P.; Jenkins, J.R.

submitted to the EMBL Data Library, August 1990

A:Reference number: S40773

A:Accession: S40773

A:Molecule type: DNA

A:Residues: 1-393 <CHU>

A:Cross-references: UNIPARC:UPI000006F8F0; EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PI

R:Matlaszewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol, S.

EMBO J. 3, 3257-3262, 1984

A:Title: Isolation and characterization of a human p53 cDNA clone: expression of the hum

A:Reference number: S42669; MUID:85126934; PMID:6396087

A:Accession: S42669

A:Molecule type: mRNA

A:Residues: 101-393 <MK13>

A:Cross-references: UNIPARC:UPI000016A844; EMBL:X01405; NID:g35215; PIDN:CAA25652.1; PI

R:Dakht-Houri, R.; Biern-Tadmor, B.; Givoli, D.; Oren, M.

EMBO J. 4, 1251-1255, 1985

A:Title: Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells.

A:Reference number: A22837; MUID:85230577; PMID:406916

A:Accession: A22837

A:Molecule type: mRNA

A:Residues: 1-71, 'P', 73-393 <ZAK>

A:Cross-references: UNIPARC:UPI000002ED67; EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CA

R:Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.

Mol. Cell. Biol. 5, 1601-1610, 1985

A:Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tu

A:Reference number: A55060; MUID:85267676; PMID:3894933

A:Accession: A55060

A:Molecule type: mRNA

A:Residues: 1-71, 'P', 73-272, 'H', 274-393 <HAR>

A:Cross-references: UNIPARC:UPI000014AB2; GB:K03199; NID:g189478; PIDN:AAA59989.1; PI

R:Harlow, N.; Billi, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.; Rotter, V.

Mol. Cell. Biol. 6, 4650-4656, 1986

A:Title: Molecular basis for heterogeneity of the human p53 protein.

A:Reference number: A93086; MUID:87089826; PMID:3025664

A:Accession: A25397

A:Molecule type: mRNA

A:Residues: 1-78, 'T', 80-393 <HAR1>

A:Cross-references: UNIPARC:UPI00001409D; EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PI

A:Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line

A:Accession: B25397

A:Molecule type: mRNA

A:Residues: 1-71, 'P', 73-78, 'T', 80-393 <HAR2>

A:Cross-references: UNIPARC:UPI0000031A0; EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PI

A:Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line

R:Matlaszewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, L.V.

Mol. Cell. Biol. 7, 961-966, 1987

A:Title: Primary structure polymorphism at amino acid residue 72 of human p53.

A:Reference number: S42452; MUID:8714273; PMID:3547088

A:Accession: S42452

A:Molecule type: DNA

A:Residues: 66-71, 'P', 73-79 <MK12>

A:Cross-references: UNIPARC:UPI00001739B5

A:Experimental source: clone lambda C113

A>Note: 72-Cys was also found, and appears to represent a polymorphism

A:Accession: S42453

A:Molecule type: mRNA, DNA

A:Residues: 66-79 <MK13>

A:Cross-references: UNIPARC:UPI00001739B6

A:Experimental source: clone J6K

R:Farrell, P.J.; Allan, G.J.; Shanahan, F.; Voutsden, K.H.; Crook, T.

EMBO J. 10, 2879-2887, 1991

A:Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.

A:Reference number: I38082; MUID:92007731; PMID:1915267

A:Accession: I38082

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-189, 'L', 190-393 <F01>

A:Cross-references: UNIPARC:UPI000011F824; EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PI

A>Note: deletion of a C nucleotide causes a frameshift at position 566

A:Accession: I38083

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-192, 'R', 194-393 <F02>

A:Cross-references: UNIPARC:UPI0000070FCE; EMBL:X60011; NID:g506434; PIDN:CAA42626.1; PI

A:Accession: I38084

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-393 <F03>

A:Cross-references: UNIPARC:UPI000006F8F0; EMBL:X60012; NID:g506436; PIDN:CAA42627.1; PI

A:Accession: I38085

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-245, 'T', 247-393 <F04>

A:Cross-references: UNIPARC:UPI000006CF84; EMBL:X60013; NID:g506438; PIDN:CAA42628.1; PI

A:Accession: I38086

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-236, 'T', 238-393 <F05>

A:Cross-references: UNIPARC:UPI0000072B7; EMBL:X60014; NID:g506440; PIDN:CAA42629.1; PI

A:Accession: I38087

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-247, 'Q', 249-393 <F06>

A:Cross-references: UNIPARC:UPI0000072FD4; EMBL:X60015; NID:g506442; PIDN:CAA42630.1; PI

A:Accession: I38088

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-247, 'Q', 249-393 <F08>

A:Cross-references: UNIPARC:UPI0000072FD4; EMBL:X60017; NID:g506446; PIDN:CAA42632.1; PI

A:Accession: I38090

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>

A:Cross-references: UNIPARC:UPI00000755C; EMBL:X60018; NID:g506448; PIDN:CAA42633.1; PI

A:Accession: I38091

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-212, 'Q', 214-393 <F10>

A:Cross-references: UNIPARC:UPI00000701E7; EMBL:X60019; NID:g506450; PIDN:CAA42634.1; PI

A:Accession: I38092

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-253, 'D', 255-393 <F11>

A:Cross-references: UNIPARC:UPI000006E77E; EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PI

A>Note: all sequences submitted to the EMBL/GenBank/DBJ databases June 1991

R:Notre, P.A.; Barrett, J.C.; Wiseman, R.W.

Nucleic Acids Res. 19, 6977, 1991

A:Title: An Alu polymorphism intragenic to the TP53 gene.

A:Reference number: I38093; MUID:92107726; PMID:1762341

A:Accession: I38093

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-393 <FUT>

A:Cross-references: UNIPARC:UPI000006F8F0; EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PI

R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakatani,

Cancer Res. 51, 5800-5805, 1991

A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell line

A:Reference number: A44905; MUID:92034678; PMID:1933850

A:Accession: A44905

A:Molecule type: DNA

A:Residues: 246-247, 'W', 249-250 <YAN>

A:Cross-references: UNIPARC:UPI000011E80C; GB:S63157; NID:g237829; PIDN:AA620140.1; PI

A>Note: sequence extracted from NCBI backbone (NCBIN:63157, NCBIP:63158)

A>Note: mutation from a liver metastasis of a gastric cancer  
 R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.  
 Oncogene 6, 1067-1071, 1991  
 A>Title: Use of the single strand conformation polymorphism technique and PCR to detect  
 A:Reference number: 158354; MUID:91296386; PMID:1648702  
 A:Accession: 158354  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 244-247, 'W', 249-252 <HENT>  
 A:Cross-references: UNIPARC:UPI000011F7CC; GB:S41969; NID:G1679931; PIDN:AAB19324.1; PIT  
 A:Accession: 178850  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 274-277, 'S', 279-282 <HENT>  
 A:Cross-references: UNIPARC:UPI000011F7CD; GB:S41977; NID:G1679932; PIDN:AAB19325.1; PIT  
 R:Chow, V.T.; Quek, H.H.; Toock, E.P.C.  
 Cancer Lett. 73, 141-148, 1993  
 A>Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphobla  
 A:Reference number: 152681; MUID:94036762; PMID:8221626  
 A:Accession: 152681  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 327-331, 'DQTSFQENC' <CHO>  
 A:Cross-references: UNIPARC:UPI000011F7D7; GB:S66666; NID:G436292; PIDN:AAB26601.1; PID  
 A>Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lym  
 R:Peterson, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.  
 Mol. Gen. Genet. 249, 425-431, 1995  
 A>Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragme  
 A:Reference number: S60151; MUID:96133682; PMID:8552047  
 A:Accession: S60153  
 A:Molecule type: DNA  
 A:Residues: 3-44 <PER>  
 A:Cross-references: UNIPARC:UPI00001739B7

Query Match 94.3%; Score 99; DB 1; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 DB 12 PPLSQETFSDLWKLLPEN 29

## RESULT 3

S06594  
 Cellular tumor antigen p53 - green monkey  
 C/Species: Cercopithecus aethiops (green monkey, grivet)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: S06594  
 R:rigaudy, P.; Eckhart, W.  
 Nucleic Acids Res. 17, 8375, 1989  
 A>Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphoprotein p53.  
 A:Reference number: S06594; MUID:90045967; PMID:2530498  
 A:Accession: S06594  
 A:Molecule type: mRNA  
 A:Residues: 1-393 <RIG>  
 A:Cross-references: UNIPROT:P13481; UNIPARC:UPI0000131039; EMBL:X16384; NID:922795; PIDN  
 C:Superfamily: cellular tumor antigen p53  
 C/Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph  
 F:176, 179, 238, 242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
 F:192/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 94.3%; Score 99; DB 1; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 DB 12 PPLSQETFSDLWKLLPEN 29

## RESULT 4

SS1648

cellular tumor antigen p53 - bovine  
 N/Alternate names: tumor-suppressor protein p53  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: S51648  
 R:Dequiedt, F.; Willems, L.; Burny, A.; Kettmann, R.  
 submitted to the EMBL Data Library, September 1994  
 A>Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and its  
 A:Reference number: S51648  
 A:Accession: S51648  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-386 <DEQ>  
 A:Cross-references: UNIPROT:Q29628; UNIPARC:UPI0000131035; EMBL:X81704; NID:G602332; PI  
 C:Superfamily: cellular tumor antigen p53  
 C/Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein  
 F:168, 171, 231, 235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
 F:385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 89.5%; Score 94; DB 1; Length 386;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-06;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 DB 12 PPLSQETFSDLWKLLPEN 29

## RESULT 5

JC6176  
 tumor suppressor protein p53 - Chinese hamster  
 C/Species: Cricetus griseus (Chinese hamster)  
 C/Date: 11-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 09-Jul-2004  
 C/Accession: JC6176  
 R:Lee, H.; Larner, J.M.; Hamlin, J.L.  
 Gene 184, 177-183, 1997  
 A>Title: Cloning and characterization of Chinese hamster p53 cDNA.  
 A:Reference number: JC6176; MUID:97183659; PMID:9031625  
 A:Accession: JC6176  
 A:Contents: 1167  
 A:Molecule type: mRNA  
 A:Residues: 1-393 <LEB>  
 A:Cross-references: UNIPROT:O09185; UNIPARC:UPI0000170734; GB:U50395; NID:G1842229; PID  
 C:Comment: This protein is a multimer, it plays the central role in a complex DNA damage  
 iption, and recombination by protein/protein interactions.  
 C/Genetics:  
 A:Gene: p53  
 C:Superfamily: cellular tumor antigen p53  
 C/Keywords: liver; tumor

Query Match 81.9%; Score 86; DB 2; Length 393;  
 Best Local Similarity 94.1%; Pred. No. 3e-05;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPLSQETFSDLWKLLPEN 18  
 |||||  
 DB 13 PPLSQETFSDLWKLLPEN 29

## RESULT 6

JH0633  
 cellular tumor antigen p53 - golden hamster  
 N/Alternate names: tumor-suppressor protein p53  
 C/Species: Mesocricetus auratus (golden hamster)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: JH0633  
 R:Legros, Y.; McIntyre, P.; Soussi, T.  
 Gene 112, 247-250, 1992  
 A>Title: The cDNA cloning and immunological characterization of hamster p53.  
 A:Reference number: JH0633; MUID:92210007; PMID:1555773  
 A:Accession: JH0633  
 A:Molecule type: mRNA  
 A:Residues: 1-396 <LEG>

A:Cross-references: UNIPROT:Q00366; UNIPARC:UPI0000131042; GB:M75144; NID:g191414; PIDN:  
A:Experimental source: Kidney, strain MPI  
C:Genetics:  
A:Gene: p53  
C:Superfamily: cellular tumor antigen p53  
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph  
F:179,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 81.9%; Score 86; DB 1; Length 396;  
Best Local Similarity 94.1%; Pred. No. 3e-05;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLLPEN 18  
Db 13 PLSQETFSDLWKLLPEN 29

RESULT 7  
A29376  
cellular tumor antigen p53 - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A29376; S61531; S72313; I51639  
R:Sousai, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.  
Oncogene 1, 71-78, 1987  
A:Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a protein  
A:Reference number: A29376; M0ID:88134684; PMID:2830576  
A:Accession: A29376  
A:Molecule type: mRNA  
A:Residues: 1-363 <SOU>  
A:Cross-references: UNIPROT:P07193; UNIPARC:UPI0000131040; EMBL:X05191; NID:g64961; PIDN:  
R:Hoever, M.; Clement, U.H.; Wedlich, D.; Montenath, M.; Knoechel, W.  
Oncogene 9, 109-120, 1994  
A:Title: Overexpression of wild-type p53 interferes with normal development in Xenopus  
A:Reference number: I51639; M0ID:94134403; PMID:8302570  
A:Accession: S61531  
A:Molecule type: mRNA  
A:Residues: 1-293,295-363 <HOE>  
A:Cross-references: UNIPARC:UPI0000171479; EMBL:X77546; NID:g468513; PIDN:CAAS4672.1; PI  
R:Hoever, M.; Clement, U.; Wedlich, D.; Montenath, M.; Knoechel, W.  
submitted to the EMBL Data Library, March 1994  
A:Reference number: S72313  
A:Accession: S72313  
A:Molecule type: mRNA  
A:Residues: 1-51, 'S', 53-70, 72-293, 295-363 <HOW>  
A:Cross-references: UNIPARC:UPI000171595; EMBL:X77546; NID:g468513; PIDN:CAAS4672.1; PI  
C:Genetics:  
A:Gene: p53  
C:Superfamily: cellular tumor antigen p53  
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph  
F:150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 77.1%; Score 81; DB 1; Length 363;  
Best Local Similarity 82.4%; Pred. No. 0.00016;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPE 17  
Db 11 PPLSQETFSDLWKLLPE 27

RESULT 8  
S38824  
cellular tumor antigen p53, minor splice form - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S38824; S35478  
R:Rat, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.  
Mol. Cell. Biol. 6, 3232-3239, 1986  
A:Title: Immunologically distinct p53 molecules generated by alternative splicing.  
A:Reference number: S38822; M0ID:87064640; PMID:3023970

A:Accession: S38824  
A:Molecule type: mRNA  
A:Residues: 1-381 <ARA>  
A:Cross-references: UNIPARC:UPI000016CF91; GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:  
R:Han, K.A.; Kulesz-Martin, M.F.  
Nucleic Acids Res. 20, 1979-1981, 1992  
A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different tis  
A:Reference number: S35478; M0ID:92253421; PMID:1579500  
A:Accession: S35478  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-381 <HAN>  
A:Cross-references: UNIPARC:UPI000016CF91; EMBL:M13874; NID:g200202; PIDN:AAA39883.1; P  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988  
A:Comment: This sequence, produced by alternative splicing of the tenth intron, lacks th  
s not known.

C:Superfamily: cellular tumor antigen p53  
C:Keywords: alternative splicing; phosphoprotein; zinc  
F:1-44/Domain: transcription activation #status predicted <TRA>  
F:16-26/Region: conserved region I  
F:99-289/Domain: DNA-binding core #status predicted <DBC>  
F:108-121/Region: L1 loop  
F:114-139/Region: conserved region II  
F:160-192/Region: L2 loop  
F:168-178/Region: conserved region III  
F:231-252/Region: conserved region IV  
F:233-248/Region: L3 loop  
F:267-283/Region: conserved region V  
F:313-319/Region: nuclear location signal  
F:319-357/Region: tetramer association  
F:7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted  
F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
F:312/Binding site: phosphate (Ser) (covalent) (by cdck2 kinase) #status predicted

Query Match 70.5%; Score 74; DB 2; Length 381;  
Best Local Similarity 93.3%; Pred. No. 0.0019;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLLP 16  
Db 16 PLSQETFSGLWKLLP 30

RESULT 9  
DNMS53  
cellular tumor antigen p53 - mouse  
N:Alternate names: oncoprotein p53  
C:Species: Mus musculus (house mouse)  
C>Date: 28-Aug-1985 #sequence\_revision 04-Oct-1996 #text\_change 09-Jul-2004  
C:Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703  
R:Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.  
EMBO J. 3, 2179-2183, 1984  
A:Title: Analysis of the gene coding for the murine cellular tumour antigen p53.  
A:Reference number: A22739; M0ID:85027173; PMID:6092064  
A:Accession: A22739  
A:Molecule type: DNA  
A:Residues: 1-134, 'V', 136-390 <BTE>  
A:Cross-references: UNIPROT:P02340; UNIPARC:UPI00001449CC; GB:X00876; NID:g871420; PIDN:  
R:Chumakov, P.M.  
Bioorg. Khim. 13, 1691-1694, 1987  
A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.  
A:Reference number: S06336; M0ID:88221682; PMID:3329909  
A:Accession: S06336  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-134, 'V', 136-390 <CHU>  
A:Cross-references: UNIPARC:UPI00001449CC  
R:Rakut-Houri, R.; Oren, M.; Bienz, B.; Lavie, V.; Hazum, S.; Givol, D.  
Nature 306, 594-597, 1983  
A:Title: A single gene and a pseudogene for the cellular tumour antigen p53.  
A:Reference number: A02684; M0ID:84068204; PMID:6646235  
A:Accession: A02684  
A:Molecule type: mRNA

A;Residues: 1-159, 'H', 161-167, 'G', 169-233, 'I', 235-390 <ZAK>  
 A;Cross-references: UNIPARC:UPI00000173988; GB:X01237; GB:K01700; NID:G53575  
 R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.  
 Mol. Cell. Biol. 6, 3232-3239, 1986  
 A;Title: Immunologically distinct p53 molecules generated by alternative splicing.  
 A;Reference number: S38822; MUID:67064640; PMID:3023970  
 A;Accession: S38822  
 A;Molecule type: mRNA  
 A;Residues: 1-390 <ARA1>  
 A;Cross-references: UNIPARC:UPI00000002B3; EMBL:M13872; NID:G200198; PIDN:AAA39881.1; PI  
 A;Accession: S38823  
 A;Molecule type: mRNA  
 A;Residues: 1-167, 'G', 169-233, 'I', 235-390 <ARA2>  
 A;Cross-references: UNIPARC:UPI00000173989; EMBL:M13873  
 R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.  
 submitted to the EMBL Data Library, July 1988  
 A;Reference number: S40014  
 A;Accession: S40014  
 A;Molecule type: mRNA  
 A;Residues: 1-167, 'G', 169-390 <ARA3>  
 A;Cross-references: UNIPARC:UPI000016CF90; EMBL:M13873; NID:G200200; PIDN:AAA39882.1; PI  
 R;denkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.  
 Nucleic Acids Res. 12, 5609-5626, 1984  
 A;Title: Cloning and expression analysis of full length mouse cDNA sequences encoding th  
 A;Reference number: 148703; MUID:84272240; PMID:6379601  
 A;Accession: 148703  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-47, 'R', 49-78, 'QW', 82-390 <RES>  
 A;Cross-references: UNIPARC:UPI000016CF8F; EMBL:X00741; NID:G53570; PIDN:CAA25323.1; PI  
 C;Comment: This DNA-binding protein plays an essential role in the regulation of cell di  
 C;Comment: The tetramer association region may exhibit a beta-turn, beta-sheet, beta-tu  
 C;Superfamily: cellular tumor antigen p53  
 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;  
 F;1-44/Domain: transcription activation #status predicted <TRA>  
 F;16-26/Region: conserved region I  
 F;99-289/Domain: DNA-binding core #status predicted <DBC>  
 F;108-121/Region: L1 loop  
 F;114-139/Region: conserved region II  
 F;160-192/Region: L2 loop  
 F;168-178/Region: conserved region III  
 F;231-252/Region: conserved region IV  
 F;233-248/Region: L3 loop  
 F;267-283/Region: conserved region V  
 F;313-319/Region: nuclear location signal  
 F;319-557/Region: tetramer association  
 F;7,9,12,18,22,37/Binding site: phosphate (Ser) (covalent) #status predicted  
 F;173,176,235,239/Binding site: zinc (Cys, His, Cys) #status predicted  
 F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted  
 F;389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 70.5%; Score 74; DB 1; Length 390;  
 Best Local Similarity 93.3%; Pred. No. 0.0019;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLP 16  
 DB 16 PLSQETFSGLWKLP 30

RESULT 10

S02192  
 cellular tumor antigen p53 - rat  
 N;Alternate names: gene p53 protein; nuclear oncoprotein p53  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: S02192; S41149  
 R;Soussi, T.; de Fromental, C.C.; Breugnot, C.; May, E.  
 Nucleic Acids Res. 16, 11384, 1988  
 A;Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.  
 A;Reference number: S02192; MUID:89083585; PMID:3060862  
 A;Accession: S02192  
 A;Molecule type: mRNA

A;Residues: 1-391 <SOU>  
 A;Cross-references: UNIPROT:P10361; UNIPARC:UPI00000131048; EMBL:X13058; NID:G56828; PID  
 R;Hulla, J.E.; Schneider, R.P.  
 Nucleic Acids Res. 21, 713-717, 1993  
 A;Title: Structure of the rat p53 tumor suppressor gene.  
 A;Reference number: S41149; MUID:93181268; PMID:8441680  
 A;Accession: S41149  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-173, 'W', 175-391 <HUL>  
 A;Cross-references: UNIPARC:UPI00000167989; EMBL:L07909  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992  
 C;Genetic: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2  
 A;Intons: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2  
 C;Superfamily: cellular tumor antigen p53  
 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph  
 F;174,177,236,240/Binding site: zinc (Cys, His, Cys) #status predicted  
 F;390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 68.6%; Score 72; DB 1; Length 391;  
 Best Local Similarity 93.3%; Pred. No. 0.0039;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLP 16  
 DB 13 PLSQETFSGLWKLP 27

RESULT 11

JH0631  
 cellular tumor antigen p53 - rainbow trout  
 C;Species: Oncorhynchus mykiss (rainbow trout)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: JH0631  
 R;de Fromental, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.  
 Gene 112, 241-245, 1992  
 A;Title: Rainbow trout p53: cDNA cloning and biochemical characterization.  
 A;Reference number: JH0631; MUID:92210006; PMID:1339362  
 A;Accession: JH0631  
 A;Molecule type: mRNA  
 A;Residues: 1-396 <DEP>  
 A;Cross-references: UNIPROT:P25035; UNIPARC:UPI00000131043; GB:M75145; NID:G213828; PIDN  
 A;Experimental source: liver  
 C;Comment: This protein is the product of a tumor suppressor gene, p53, whose inactivat  
 C;Superfamily: cellular tumor antigen p53  
 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph  
 F;164,167,227,231/Binding site: zinc (Cys, His, Cys) #status predicted  
 F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 57.1%; Score 60; DB 1; Length 396;  
 Best Local Similarity 76.9%; Pred. No. 0.26;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLP 14  
 DB 11 PLSQBSFBDLWKX 23

RESULT 12

S28857  
 glutamate receptor delta-1 chain precursor - rat  
 N;Alternate names: kainate receptor  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 31-Dec-2004  
 C;Accession: S28857; S31222  
 R;Lomeli, H.; Sprengel, R.; Laurie, D.J.; Koehn, G.; Herb, A.; Seeburg, P.H.; Wisden, W  
 FEBS Lett. 315, 318-322, 1993  
 A;Title: The rat delta-1 and delta-2 subunits extend the excitatory amino acid receptor  
 A;Reference number: S28857; MUID:93138096; PMID:8422924  
 A;Accession: S28857  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-1009 <LOM>

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A:Cross-references: UNIPARC:UPI0000177961; EMBL:Z17238
R:Spiegel, R.
submitted to the EMBL Data Library, October 1992
A:Reference number: S31222
A:Accession: S31222
A:Molecule type: mRNA
A:Residues: 83-1009 <SPR>
A:Cross-references: UNIPARC:UPI0000170981; EMBL:Z17238; NID:gs56285; PIDN:CAA78936.1; PID
C:Superfamily: mannose 6-phosphate receptor, cation-independent; glutamate receptor homoc
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein
F:1-15/Domain: signal sequence #status predicted <Sig>
F:16-1009/Product: glutamate receptor delta-1 chain #status predicted <MAT>
F:441-866/Domain: glutamate receptor homology <GRH>
F:565-584/Domain: transmembrane #status predicted <TM1>
F:601-621/Domain: transmembrane #status predicted <TM2>
F:632-654/Domain: transmembrane #status predicted <TM3>
F:830-851/Domain: transmembrane #status predicted <TM4>
F:422/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match          49.0%; Score 51.5; DB 2; Length 1009;
Best Local Similarity 47.4%; Pred. No. 13;
Matches 9; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 2 PLSQF-TFSDLMKLPENG 19
DB 698 PLEQDSTFAIWKRTSKNG 716

RESULT 13
JH0266
glutamate receptor delta-1 chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C:Accession: JH0266
R:Yamazaki, M.; Araki, K.; Shibata, A.; Mishina, M.
Biochem. Biophys. Res. Commun. 183, 886-892, 1992
A:Title: Molecular cloning of a cDNA encoding a novel member of the mouse glutamate rece
A:Reference number: JH0266; MUID:92198486; PMID:1372507
A:Accession: JH0266
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1009 <YAM>
A:Cross-references: UNIPROT:O61627; UNIPARC:UPI0000028BED; DDBJ:D10171; NID:9220417; PID
C:Comment: Glutamate receptor channels mediate most of the fast excitatory synaptic tran
C:Superfamily: mannose 6-phosphate receptor, cation-independent; glutamate receptor homoc
C:Keywords: glycoprotein; neurotransmitter receptor; phosphoprotein; transmembrane prote
F:1-15/Domain: signal sequence #status predicted <Sig>
F:16-1009/Product: glutamate receptor channel delta-1 chain #status predicted <GLU>
F:441-866/Domain: glutamate receptor homology <GRH>
F:565-584/Domain: transmembrane #status predicted <TM1>
F:603-621/Domain: transmembrane #status predicted <TM2>
F:632-650/Domain: transmembrane #status predicted <TM3>
F:831-851/Domain: transmembrane #status predicted <TM4>
F:131-200,422,498/Binding site: carbonylate (Asn) (covalent) #status predicted
F:593,713/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match          49.0%; Score 51.5; DB 2; Length 1009;
Best Local Similarity 47.4%; Pred. No. 13;
Matches 9; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 2 PLSQF-TFSDLMKLPENG 19
DB 698 PLEQDSTFAIWKRTSKNG 716

RESULT 14
C64396
precorrin-2 methyltransferase homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 05-Oct-2004
C:Accession: C64396
R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirsch, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;

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son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:868087
A:Accession: C64396
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-230 <BLU>
A:Cross-references: UNIPROT:O58181; UNIPARC:UPI0000139CA2; GB:U67522; GB:L77117; NID:928
C:Genetics:
C:Genetics:
A:Map position: FOR691742-692434
A:Start codon: GTG
C:Superfamily: precorrin-2 C20-methyltransferase

Query Match          47.6%; Score 50; DB 2; Length 230;
Best Local Similarity 55.6%; Pred. No. 4;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 PLSQF-TFSDLMKLPENG 19
DB 101 PLYSTFSTYWKLRG 118

RESULT 15
G86715
racemase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86715
R:Boletín, A.; Winkler, P.; Mauger, S.; Jallón, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86715
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-367 <STO>
A:Cross-references: UNIPROT:Q9CHK4; UNIPARC:UPI00000068C4; GB:AE005176; PID:G12723640; I
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yhb8

Query Match          47.6%; Score 50; DB 2; Length 367;
Best Local Similarity 52.9%; Pred. No. 7;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 PLSQF-TFSDLMKLPENG 17
DB 54 PLYSTFSTYWKLRG 70

Search completed: July 5, 2006, 22:46:31
Job time : 41 secs

```

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 5, 2006, 22:37:36 ; Search time 295 Seconds  
(Without alignments)  
59.577 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSFDMKLPEN 19

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprot:\*  
2: uniprot\_tramb1:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	94.3	39	2 061T77_HUMAN	061T77 homo sapien
2	99	94.3	341	2 03LRW5_HUMAN	03LRW5 homo sapien
3	99	94.3	346	2 03LRW4_HUMAN	03LRW4 homo sapien
4	99	94.3	386	1 P53_PIG	091ub2 sus scrofa
5	99	94.3	387	1 P53_DELLE	08SPZ3 delphinapte
6	99	94.3	391	1 P53_CAVPO	09Wp26 cavia porce
7	99	94.3	391	1 P53_RABIT	095330 corycolagus
8	99	94.3	393	1 P53_CERAE	P13481 cercopithec
9	99	94.3	393	1 P53_HUMAN	P04637 homo sapien
10	99	94.3	393	1 P53_MACFA	P64643 macaca fasc
11	99	94.3	393	1 P53_MACFU	P61260 macaca fusc
12	99	94.3	393	1 P53_MACMU	P56424 macaca mula
13	99	94.3	393	1 P53_TUPGB	091tal tupaiia glis
14	99	94.3	393	2 05UD84_HUMAN	05UD84 homo sapien
15	99	94.3	393	2 02XN98_HUMAN	02XN98 homo sapien
16	99	94.3	393	2 02XS07_HUMAN	02XS07 homo sapien
17	96	91.4	391	2 068VB0_SPAUD	068VB0 spalax juda
18	94	89.5	382	1 P53_SHEEP	P51664 ovis aries
19	94	89.5	386	1 P53_BOSTN	P67938 bos indicus
20	94	89.5	386	1 P53_BOVIN	P67939 bos taurus
21	94	89.5	386	1 03ZCF1_BOVIN	03ZCF1 bos taurus
22	94	89.5	387	2 09N252_PIG	09N252 sus scrofa
23	94	89.5	391	1 P53_MARMO	036006 marmota mon
24	90	85.7	381	1 P53_CANPA	029537 canis famli
25	90	85.7	386	1 P53_PELCA	P1685 felis silve
26	88	83.8	390	2 092DY0_MERUN	092DY0 meriones un
27	86	81.9	393	1 P53_CRIGR	009185 cricetus
28	86	81.9	396	1 P53_MESAU	000366 mesocricetu
29	81	77.1	362	2 05XHJ3_XENLA	05XHJ3 xenopus lae
30	81	77.1	362	2 06NTF1_XENTR	06NTF1 xenopus tro
31	81	77.1	362	2 07TID0_XENLA	07TID0 xenopus lae

32	81	77.1	363	1 P53_XENLA	P07193 xenopus lae
33	74	70.5	307	2 09ER40_MOUSE	09ER40 mus musculu
34	74	70.5	314	2 08C526_MOUSE	08C526 m 0 day neo
35	74	70.5	357	2 03UGQ1_MOUSE	03UGQ1 mus musculu
36	74	70.5	378	2 05F218_MOUSE	05F218 mus musculu
37	74	70.5	381	2 080ZAL_MOUSE	080ZAL mus musculu
38	74	70.5	387	2 05F217_MOUSE	05F217 mus musculu
39	74	70.5	390	1 P53_MOUSE	P02340 mus musculu
40	74	70.5	390	2 070366_MOUSE	070366 mus musculu
41	74	70.5	390	2 0549C9_MOUSE	0549C9 mus musculu
42	74	70.5	391	2 091XH8_MOUSE	091XH8 mus musculu
43	72	68.6	170	2 09EP92_RAT	09EP92 rattus norv
44	72	68.6	271	2 09EOL0_RAT	09EOL0 rattus norv
45	72	68.6	391	1 P53_RAT	P10361 rattus norv

#### ALIGNMENTS

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RESULT 1
061T77_HUMAN      PRELIMINARY;  PRT;    39 AA.
AC  061T77;
DT  05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT  05-JUL-2004, sequence version 1.
DT  07-FEB-2006, entry version 6.
DE  P53 tumor suppressor (fragment) .
OS  Homo sapiens (Human) .
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC  Homo
OX  NCBI_TaxID=9606;
RN  [1]
RP  NCLEBOTIDE SEQUENCE.
RA  Ray P.S., Grover R., Das S.;
RU  Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NonDerivs License
CC  -----
DR  EMBL; AY627884; AAT940418.1; -; mRNA.
DR  Ensembl; ENSG00000141510; Homo sapiens.
FT  NON TER
SQ  SEQUENCE 39 AA; 4351 MW; EFAAE80444CE8A30 CRC64;
Query Match 94.3%; Score 99; DB 2; length 39;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 PPLSQETFSFDMKLPEN 18
Db  12 PPLSQETFSFDMKLPEN 29

RESULT 2
03LRW5_HUMAN      PRELIMINARY;  PRT;    341 AA.
AC  03LRW5;
DT  25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT  25-OCT-2005, sequence version 1.
DT  07-FEB-2006, entry version 5.
DE  P53 beta isoform.
GN  Name=P53;
OS  Homo sapiens (Human) .
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC  Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  NCLEBOTIDE SEQUENCE.
RA  PubMed=16131611; DOI=10.1101/gad.1339905;
RA  Bourdon J.C., Fernandes K., Murray-Zmijewski F., Liu G., Diot A.,
RA  Xiroltimas D.P., Saville M.K., Lane D.P.;
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RT      "p53 isoforms can regulate p53 transcriptional activity."
RL      Genes Dev. 19:2122-2137(2005).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RA      Bourdon J.-C.R., Fernandes K., Lane D.;
RL      Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC      -----
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CC      Distributed under the Creative Commons Attribution-NonDerivs license
CC      -----
DR      EMBL; DQ186648; ABA29753.1; -; mRNA.
DR      GO; GO:0005634; C:nucleus; IEA.
DR      GO; GO:0046872; F:metal ion binding; IEA.
DR      GO; GO:0003700; F:transcription factor activity; IEA.
DR      GO; GO:0008270; F:zinc ion binding; IEA.
DR      GO; GO:0006915; P:apoptosis; IEA.
DR      GO; GO:0007049; P:cell cycle; IEA.
DR      GO; GO:0045786; P:negative regulation of progression through . . .; IEA.
DR      GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR      GO; GO:0006350; P:transcription; IEA.
DR      InterPro; IPR002117; P53.
DR      Pfam; PF00870; P53; 1.
DR      ProDom; PD002681; P53; 1.
DR      PRINTS; PR00386; P53SUPPRESSR.
DR      PROSITE; PS00348; P53; 1.
DR      Activator; Anti-oncogene; Apoptosis; Cell cycle; DNA-binding;
KW      Metal-binding; Nuclear protein; Phosphorylation; Transcription;
KW      Transcription regulation; Zinc.
SQ      SEQUENCE 341 AA; 37885 MW; 2C5E71634A57F461 CRC64;

Query Match          94.3%; Score 99; DB 2; Length 341;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PPLSQETFSDLWKLPEN 18
DB      12 PPLSQETFSDLWKLPEN 29

RESULT 3
O3LRM4 HUMAN PRELIMINARY; PRT; 346 AA.
AC      O3LRM4;
DT      25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT      07-FEB-2006, entry version 1.
DE      P53 gamma isoform.
GN      Name=TP53;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RA      Pubmed=16131611; DOI=10.1101/gad.1339905;
RA      Bourdon J.C., Fernandes K., Murray-Zmijewski F., Liu G., Diot A.,
RA      Xirodimas D.P., Saville M.K., Lane D.P.;
RT      "p53 isoforms can regulate p53 transcriptional activity."
RL      Genes Dev. 19:2122-2137(2005).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RA      Bourdon J.-C.R., Fernandes K., Lane D.;
RL      Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs license
CC      -----
DR      EMBL; DQ186649; ABA29754.1; -; mRNA.
DR      GO; GO:0005634; C:nucleus; IEA.
DR      GO; GO:0046872; F:metal ion binding; IEA.
DR      GO; GO:0003700; F:transcription factor activity; IEA.

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DR      GO; GO:0008270; F:zinc ion binding; IEA.
DR      GO; GO:0006915; P:apoptosis; IEA.
DR      GO; GO:0007049; P:cell cycle; IEA.
DR      GO; GO:0045786; P:negative regulation of progression through . . .; IEA.
DR      GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR      GO; GO:0006350; P:transcription; IEA.
DR      InterPro; IPR002117; P53.
DR      InterPro; IPR011615; P53_DNA_bd.
DR      Pfam; PF00870; P53; 1.
DR      PRINTS; PR00386; P53SUPPRESSR.
DR      ProDom; PD002681; P53; 1.
DR      PROSITE; PS00348; P53; 1.
KW      Activator; Anti-oncogene; Apoptosis; Cell cycle; DNA-binding;
KW      Metal-binding; Nuclear protein; Phosphorylation; Transcription;
KW      Transcription regulation; Zinc.
SQ      SEQUENCE 346 AA; 38501 MW; 6F18E09F8CD9129F CRC64;

Query Match          94.3%; Score 99; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PPLSQETFSDLWKLPEN 18
DB      12 PPLSQETFSDLWKLPEN 29

RESULT 4
P53_PIG
ID      P53_PIG STANDARD; PRT; 386 AA.
AC      Q9TUB2;
DT      01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
DT      01-MAY-2000, sequence version 1.
DT      07-FEB-2006, entry version 52.
DE      Cellular tumor antigen p53 (Tumor suppressor p53).
GN      Name=TP53; Synonyms=P53;
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC      Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RA      MEDLINE=99422034; Pubmed=10490836; DOI=10.1038/sj.onc.1202870;
RA      Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;
RT      "Nucleotide sequence of the porcine p53 cDNA, and the detection of
RT      recombinant porcine p53 expressed in vitro with a variety of anti-p53
RT      antibodies."
RL      Oncogene 18:5005-5009(1999).
CC      -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC      growth arrest or apoptosis depending on the physiological
CC      circumstances and cell type. Involved in cell cycle regulation as
CC      a trans-activator that acts to negatively regulate cell division
CC      by controlling a set of genes required for this process. One of
CC      the activated genes is an inhibitor of cyclin-dependent kinases.
CC      Apoptosis induction seems to be mediated either by stimulation of
CC      BAX and FAS antigen expression, or by repression of Bcl-2
CC      expression.
CC      -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC      -1- SUBUNIT: Binds DNA as a homotrimer. Found in a complex with
CC      CABLES1 and p53/TP73. Interacts with histone acetyltransferases
CC      EP300 and methyltransferases HR23L2 and CARM1, and recruits them
CC      to promoters. C-terminus interacts with TAF1, when TAF1 is part of
CC      the TFIID complex. Interacts with HIPK1, HIPK2, AXIN1, and
CC      PS3DINP1. Part of a complex consisting of TP53, HIPK2 and AXIN1.
CC      Interacts with WWOX (By similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC      -1- PTM: Phosphorylated. Phosphorylation on Ser residues mediates
CC      transcriptional activation. Phosphorylated on Thr-18 by VRK1,
CC      which may prevent the interaction with MDM2. Phosphorylated by
CC      HIPK1 (By similarity).
CC      -1- PTM: Acetylated. Its deacetylation by SIRT1 impairs its ability to
CC      induce proapoptotic program and modulate cell senescence (By
CC      similarity).

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CC -1- DISEASE: p53 is found in increased amounts in a wide variety of
CC transformed cells. p53 is frequently mutated or inactivated in
CC many types of cancer.
CC -1- SIMILARITY: Belongs to the p53 family.
CC -----
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CC -----
DR EMBL: AF098067; AAF04620.1; -; mRNA.
DR HSSP: P04637; 1GZH.
DR SMR: Q9TUB2; 86-282.
DR GO: GO:0005739; C:mitochondrion; ISS.
DR GO: GO:0005730; C:nucleolus; ISS.
DR GO: GO:0005524; F:ATP binding; ISS.
DR GO: GO:0005507; F:copper ion binding; ISS.
DR GO: GO:0003677; F:DNA binding; ISS.
DR GO: GO:0000739; F:DNA strand annealing activity; ISS.
DR GO: GO:0005515; F:protein binding; ISS.
DR GO: GO:0006915; F:apoptosis; ISS.
DR GO: GO:0006284; F:base-excision repair; ISS.
DR GO: GO:0008635; F:caspase activation via cytochrome c; ISS.
DR GO: GO:0007569; P:cell aging; ISS.
DR GO: GO:0007050; P:cell cycle arrest; ISS.
DR GO: GO:0030154; P:cell differentiation; ISS.
DR GO: GO:0008283; P:cell proliferation; ISS.
DR GO: GO:0030308; P:negative regulation of cell growth; ISS.
DR GO: GO:0006289; P:nucleotide-excision repair; ISS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR011615; P53_DNA_bd.
DR InterPro: IPR012346; P53_RUNT_DNA_bd.
DR InterPro: IPR010991; P53_tetramer1strn.
DR Pfam: PF00870; P53_1.
DR Pfam: PF07710; P53_tetramer; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR POSITE: PS00348; P53; 1.
DR Acetylacton: Activator; Anti-oncogene; Apoptosis; Cell cycle;
KW DNA-binding; Metal-binding; Nuclear protein; Phosphorylation;
KW Transcription; Transcription regulation; Zinc.
FT CHAIN 1 386
FT DNA BIND 94 285
FT REGION 1 45 Transcription activation (acidic).
FT REGION 63 102 Interaction with WMX (By similarity).
FT REGION 92 363 Interaction with HIRK1 (By similarity).
FT REGION 108 285 Interaction with AXIN1 (By similarity).
FT REGION 312 353 Interaction with HIPK2 (By similarity).
FT REGION 318 349 Oligomerization.
FT REGION 361 380 Basic (repression of DNA-binding).
FT MOTIF 298 314 Bipartite nuclear localization signal (By
FT similarity).
FT MOTIF 332 343 Nuclear export signal (By similarity).
FT METAL 168 168 Zinc (By similarity).
FT METAL 171 171 Zinc (By similarity).
FT METAL 231 231 Zinc (By similarity).
FT METAL 235 235 Zinc (By similarity).
FT BINDING 385 385 5'-phospho-RNA (covalent) (By
FT similarity).
FT MOD_RES 15 15 Phosphoserine (by PPPK) (By similarity).
FT MOD_RES 18 18 Phosphothreonine (by VRK1) (By
FT similarity).
FT MOD_RES 298 298 N6-acetyllysine (By similarity).
FT MOD_RES 366 366 N6-acetyllysine (By similarity).
FT MOD_RES 375 375 N6-acetyllysine (By similarity).
SQ SEQUENCE 386 AA; 42862 MW; A4C3D8B8BDF5162 CRC64;
Query Match 94.3%; Score 99; DB 1; Length 386;
Best Match Similarity 100.0%; Pred. No. 2.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPSQETFSDLWKLPEN 18
Db 12 PPSQETFSDLWKLPEN 29

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RESULT 5
P53_DELLE STANDARD; PRT; 387 AA.
AC 088P23;
DT 20-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN Name=TP53; Synonyms=p53;
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Leukocyte;
RX MEDLINE=22030464; Pubmed=12034505; DOI=10.1016/S0378-1119(02)00472-9;
RA Xu N., Shiraki T., Yamada T., Nakajima M., Gauthier J.M.,
RA Pfeiffer C.J., Sato S.;
RT "Nucleotide sequence of the p53 cDNA of beluga whale (Delphinapterus
RT leucas)".;
RL Gene 288:156-166 (2002).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer. Found in a complex with
CC CABES1 and p53/TP73. Interacts with histone acetyltransferases
CC EP300 and methyltransferases HMTN12 and CBAT1, and recruits them
CC to promoters. C-terminus interacts with TAF1, when TAF1 is part of
CC the TFIID complex. Interacts with HIPK1, HIPK2, AXIN1, and
CC P53DNP1. Part of a complex consisting of TP53, HIPK2 and AXIN1.
CC Interacts with WMX (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -1- PTM: Phosphorylated. Phosphorylation on Ser residues mediates
CC transcriptional activation. Phosphorylated on Thr-18 by VRK1,
CC which may prevent the interaction with MDM2. Phosphorylated by
CC HIPK1 (By similarity).
CC -1- PTM: Acetylated. Its deacetylation by SIRT1 impairs its ability to
CC induce proapoptotic program and modulate cell senescence (By
CC similarity).
CC -1- DISEASE: p53 is found in increased amounts in a wide variety of
CC transformed cells. p53 is frequently mutated or inactivated in
CC many types of cancer.
CC -1- SIMILARITY: Belongs to the p53 family.
CC -----
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CC -----
DR EMBL: AF475081; AAL83290.1; -; mRNA.
DR HSSP: O88P23; 87-283.
DR SMR: O88P23; 87-283.
DR GO: GO:0005739; C:mitochondrion; ISS.
DR GO: GO:0005730; C:nucleolus; ISS.
DR GO: GO:0005524; F:ATP binding; ISS.
DR GO: GO:0005507; F:copper ion binding; ISS.
DR GO: GO:0003677; F:DNA binding; ISS.
DR GO: GO:0000739; F:DNA strand annealing activity; ISS.
DR GO: GO:0005515; F:apoptosis; ISS.
DR GO: GO:0006915; F:protein binding; ISS.
DR GO: GO:0006284; F:base-excision repair; ISS.
DR GO: GO:0008635; F:caspase activation via cytochrome c; ISS.
DR GO: GO:0007569; P:cell aging; ISS.
DR GO: GO:0007050; P:cell cycle arrest; ISS.

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DR GO; GO:0030154; P:cell differentiation; ISS.  
 DR GO; GO:0008283; P:cell proliferation; ISS.  
 DR GO; GO:0030308; P:negative regulation of cell growth; ISS.  
 DR GO; GO:0006289; P:nucleotide-excision repair; ISS.  
 DR InterPro; IPR002117; P53.  
 DR InterPro; IPR011615; P53 DNA bd.  
 DR InterPro; IPR012346; P53 RUNT DNA bd.  
 DR InterPro; IPR010991; P53\_tetramerictn.  
 DR Pfam; PF00870; P53; 1.  
 DR Pfam; PF07710; P53\_tetramer; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR ProDom; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 DR Acetylation; Activator; Anti-oncogene; Apoptosis; Cell cycle;  
 KW DNA-binding; Metal-binding; Nuclear protein; Phosphorylation;  
 KW Transcription; Transcription regulation; Zinc.  
 FT CHAIN 1 387  
 /FtId=PRO\_0000185699.  
 FT DNA BIND 95 286  
 REGION 1 45  
 Transcription activation (acidic) (By  
 similarity).  
 FT REGION 59 103  
 REGION 93 364  
 REGION 109 286  
 REGION 313 354  
 REGION 319 350  
 REGION 362 381  
 FT MOTIF 299 315  
 Bipartite nuclear localization signal (By  
 similarity).  
 FT MOTIF 333 344  
 Nuclear export signal (By similarity).  
 FT METAL 169 169  
 Zinc (By similarity).  
 FT METAL 172 172  
 Zinc (By similarity).  
 FT METAL 232 232  
 Zinc (By similarity).  
 FT METAL 236 236  
 Zinc (By similarity).  
 FT BINDING 386 386  
 5'-phospho-RNA (covalent) (By  
 similarity).  
 FT MOD\_RES 15 15  
 Phosphoserine (by PRPK) (By similarity).  
 FT MOD\_RES 18 18  
 Phosphothreonine (by VRK1) (By  
 similarity).  
 FT MOD\_RES 299 299  
 N6-acetyllysine (By similarity).  
 FT MOD\_RES 367 367  
 N6-acetyllysine (By similarity).  
 FT MOD\_RES 376 376  
 N6-acetyllysine (By similarity).  
 SQ SEQUENCE 387 AA; 43034 MW; E4C8BDBF34A540E CRC4;  
 Query Match 94.3%; Score 99; DB 1; Length 387;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PLSQTFSDMLKLPEN 18  
 Db 12 PLSQTFSDMLKLPEN 29  
 RESULT 6  
 P53 CAVPO STANDARD; PRT; 391 AA.  
 AC Q9W0R6;  
 DT 01-DIC-2000, integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1999, sequence version 1.  
 DT 07-FEB-2006, entry version 46.  
 DE Cellular tumor antigen p53 (Tumor suppressor p53).  
 GN Name=TP53;  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 OC Hystricognathi; Caviidae; Cavia.  
 OC NCBI\_TaxId=10141;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RC TISSUE=Sp1leen;  
 RX MEDLINE=99265972; PubMed=10331945; DOI=10.1006/geno.1999.5794;  
 RA D'Erchia A.M., Pesole G., Tullio A., Saccone C., Sbisa E.;

RT "Guinea pig p53 mRNA: identification of new elements in coding and  
 RT untranslated regions and their functional and evolutionary  
 RT implications".  
 RL Genomics 58:50-64(1999).  
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
 CC growth arrest or apoptosis depending on the physiological  
 CC circumstances and cell type. Involved in cell cycle regulation as  
 CC a trans-activator that acts to negatively regulate cell division  
 CC by controlling a set of genes required for this process. One of  
 CC the activated genes is an inhibitor of cyclin-dependent kinases.  
 CC Apoptosis induction seems to be mediated either by stimulation of  
 CC BAX and FAS antigen expression, or by repression of Bcl-2  
 CC expression.  
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -1- SUBUNIT: Binds DNA as a homotetramer. Found in a complex with  
 CC CABLES1 and p53/TP73. Interacts with histone acetyltransferases  
 CC EP300 and methyltransferases HRMTL2 and CARM1, and recruits them  
 CC to promoters. C-terminus interacts with TAF1, when TAF1 is part of  
 CC the TFIID complex. Interacts with HIPK1, HIPK2, AXIN1, and  
 CC p53DINP1. Part of a complex consisting of TP53, HIPK2 and AXIN1.  
 CC Interacts with WWOX (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).  
 CC -1- PTM: Phosphorylated. Phosphorylation on Ser residues mediates  
 CC transcriptional activation. Phosphorylated on Thr-18 by VRK1,  
 CC which may prevent the interaction with MDM2. Phosphorylated by  
 CC HIPK1. Phosphorylated on Ser-46 by HIPK2 upon UV irradiation.  
 CC Phosphorylation on Ser-46 is required for acetylation by CREBBP  
 CC (By similarity).  
 CC -1- PTM: Acetylated. Its deacetylation by SIRT1 impairs its ability to  
 CC induce proapoptotic program and modulate cell senescence (By  
 CC similarity).  
 CC -1- DISEASE: p53 is found in increased amounts in a wide variety of  
 CC transformed cells. p53 is frequently mutated or inactivated in  
 CC many types of cancer.  
 CC -1- SIMILARITY: Belongs to the p53 family.  
 CC -----  
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 CC -----  
 DR EMBL; AJ009673; CAB43196.1; -; mRNA.  
 DR HSSP; P04637; IGZH.  
 DR SMR; Q9W0R6; 94-288.  
 DR GO; GO:0005739; C:nucleochondrion; ISS.  
 DR GO; GO:0005730; C:nucleolus; ISS.  
 DR GO; GO:0005524; F:ATP binding; ISS.  
 DR GO; GO:0005507; F:copper ion binding; ISS.  
 DR GO; GO:0003677; F:DNA binding; ISS.  
 DR GO; GO:0000739; F:DNA strand annealing activity; ISS.  
 DR GO; GO:0005515; F:protein binding; ISS.  
 DR GO; GO:0006915; F:apoptosis; ISS.  
 DR GO; GO:0006284; P:base-excision repair; ISS.  
 DR GO; GO:0008635; P:carboxypeptidase activation via cytochrome c; ISS.  
 DR GO; GO:0007569; P:cell aging; ISS.  
 DR GO; GO:0007050; P:cell cycle arrest; ISS.  
 DR GO; GO:0030154; P:cell differentiation; ISS.  
 DR GO; GO:0008283; P:cell proliferation; ISS.  
 DR GO; GO:0030308; P:negative regulation of cell growth; ISS.  
 DR GO; GO:0006289; P:nucleotide-excision repair; ISS.  
 DR InterPro; IPR002117; P53.  
 DR InterPro; IPR011615; P53 DNA bd.  
 DR InterPro; IPR012346; P53 RUNT DNA bd.  
 DR InterPro; IPR010991; P53\_tetramerictn.  
 DR Pfam; PF00870; P53; 1.  
 DR Pfam; PF07710; P53\_tetramer; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR ProDom; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 KW Acetylation; Activator; Anti-oncogene; Apoptosis; Cell cycle;  
 KW DNA-binding; Metal-binding; Nuclear protein; Phosphorylation;  
 KW Transcription; Transcription regulation; Zinc.  
 FT CHAIN 1 391  
 /FtId=PRO\_0000185699.  
 FT DNA BIND 100 290  
 By similarity.

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FT REGION 1 44 Transcription activation (acidic).
FT REGION 64 108 Interaction with WMOX (By similarity).
FT REGION 98 268 Interaction with HIPK1 (By similarity).
FT REGION 114 290 Interaction with AXIN1 (By similarity).
FT REGION 317 358 Interaction with HIPK2 (By similarity).
FT REGION 323 354 Oligomerization.
FT REGION 366 385 Basic (repression of DNA-binding).
FT MOTIF 303 319 Bipartite nuclear localization signal (By similarity).
FT MOTIF 337 348 Nuclear export signal (By similarity).
FT METAL 174 174 Zinc (By similarity).
FT METAL 177 177 Zinc (By similarity).
FT METAL 236 236 Zinc (By similarity).
FT METAL 240 240 Zinc (By similarity).
FT BINDING 390 390 5'-phospho-RNA (covalent) (By similarity).
FT MOD_RES 15 15 Phosphoserine (by PRPK) (By similarity).
FT MOD_RES 18 18 Phosphothreonine (by VRK1) (By similarity).
FT MOD_RES 46 46 Phosphoserine (by HIPK2) (By similarity).
FT MOD_RES 303 303 N6-acetyllysine (By similarity).
FT MOD_RES 371 371 N6-acetyllysine (By similarity).
FT MOD_RES 380 380 N6-acetyllysine (By similarity).
SQ SEQUENCE 391 AA; 43288 MM; 321DA0702383573E CRC64;

Query Match 94.3%; Score 99; DB 1; Length 391;
Best Local Similarity 100.0%; Pred. No. 2,8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLMKLLPEN 18
Db 12 PPLSQETFSDLMKLLPEN 29

RESULT 7
ID P53_RABIT STANDARD; PRT; 391 AA.
AC Q95330;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DI 01-FEB-1997, sequence version 1.
DI 07-FEB-2006, entry version 53.
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN Name=P53;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=New Zealand;
RX MEDLINE=97208869; PubMed=9055811; DOI=10.1016/S0378-1119(96)00604-X;
RA le Gao F., May P., Ronco P., Caron de Fromental C.;
RT "cDNA cloning and immunological characterization of rabbit p53.";
RL Gene 185:168-173(1997).

CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotrimer. Found in a complex with
CC CABES1 and p53/TP73. Interacts with histone acetyltransferases
CC EP300 and methyltransferases HMTL2 and CARM1, and recruits them
CC to promoters. C-terminus interacts with TAF1, when TAF1 is part of
CC the TFIID complex. Interacts with HIPK1, HIPK2, AXIN1, and
CC p53DIN1. Part of a complex consisting of TP53, HIPK2 and AXIN1.
CC Interacts with WMOX (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
```

```
CC -1- PTM: Phosphorylated. Phosphorylation on Ser residues mediates
CC transcriptional activation. Phosphorylated on Thr-18 by VRK1,
CC which may prevent the interaction with MDM2. Phosphorylated by
CC HIPK1 (By similarity).
CC -1- PTM: Acetylated. Its deacetylation by SIRT1 impairs its ability to
CC induce proapoptotic program and modulate cell senescence (By
CC similarity).
CC -1- DISEASE: p53 is found in increased amounts in a wide variety of
CC transformed cells. p53 is frequently mutated or inactivated in
CC many types of cancer.
CC -1- SIMILARITY: Belongs to the p53 family.
CC -----
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CC Distributed under the Creative Commons Attribution-NonCommercial License
CC EMBL: X90592; CA62216.1; -; mRNA.
DR PIR: JC6193; JC6193.
DR HSSP: P04637; JGZH.
DR SMR: Q95330; 91-286.
DR GO: GO:0005739; C:nucleochondrion; ISS.
DR GO: GO:0005730; C:nucleolus; ISS.
DR GO: GO:0005524; F:ATP binding; ISS.
DR GO: GO:0005507; F:copper ion binding; ISS.
DR GO: GO:0003677; F:DNA binding; ISS.
DR GO: GO:0000739; F:DNA strand annealing activity; ISS.
DR GO: GO:0005515; F:protein binding; ISS.
DR GO: GO:0006915; P:apoptosis; ISS.
DR GO: GO:0006284; P:base-excision repair; ISS.
DR GO: GO:0008635; P:caspase activation via cytochrome c; ISS.
DR GO: GO:0007569; P:cell aging; ISS.
DR GO: GO:0007050; P:cell cycle arrest; ISS.
DR GO: GO:0030154; P:cell differentiation; ISS.
DR GO: GO:0008283; P:cell proliferation; ISS.
DR GO: GO:0030308; P:negative regulation of cell growth; ISS.
DR GO: GO:0006289; P:nucleotide-excision repair; ISS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR011615; P53_DNA_bd.
DR InterPro: IPR012346; P53_RUNT_DNA_bd.
DR InterPro: IPR010991; P53_tetramer1stn.
DR Pfam: PF00870; P53; 1.
DR Pfam: PF07710; P53_tetramer; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Acetylation; Apoptosis; Cell cycle;
KW DNA-binding; Metal-binding; Nuclear protein; Phosphorylation;
KW Transcription; Transcription regulation; Zinc.
FT CHAIN 1 391 Cellular tumor antigen p53.
FT FTId=PRO_0000185711.
FT DNA_BIND 99 289 By similarity.
FT REGION 1 43 Transcription activation (acidic).
FT REGION 63 107 Interaction with WMOX (By similarity).
FT REGION 97 368 Interaction with HIPK1 (By similarity).
FT REGION 113 289 Interaction with AXIN1 (By similarity).
FT REGION 317 358 Interaction with HIPK2 (By similarity).
FT REGION 323 354 Oligomerization.
FT REGION 366 385 Basic (repression of DNA-binding).
FT MOTIF 302 319 Bipartite nuclear localization signal (By similarity).
FT MOTIF 337 348 Nuclear export signal (By similarity).
FT METAL 173 173 Zinc (By similarity).
FT METAL 176 176 Zinc (By similarity).
FT METAL 235 235 Zinc (By similarity).
FT METAL 239 239 Zinc (By similarity).
FT BINDING 390 390 5'-phospho-RNA (covalent) (By similarity).
FT MOD_RES 15 15 Phosphoserine (by PRPK) (By similarity).
FT MOD_RES 18 18 Phosphothreonine (by VRK1) (By similarity).
FT MOD_RES 302 302 N6-acetyllysine (By similarity).
FT MOD_RES 371 371 N6-acetyllysine (By similarity).
FT MOD_RES 380 380 N6-acetyllysine (By similarity).
SQ SEQUENCE 391 AA; 43435 MM; 86BD5B80B726525 CRC64;
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Query Match 94.3%; Score 99; DB 1; Length 391;  
Best Local Similarity 100.0%; Pred. No. 2.8e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 PPLSQTFSIDLWKLLEN 18  
12 PPLSQTFSIDLWKLLEN 29

Db

RESULT 8  
P53\_CERAE STANDARD; PRT; 393 AA.  
AC P13481;  
DT 01-JUN-1990, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-1990, sequence version 1.  
DE 07-FEB-2006, entry version 62.  
DE Cellular tumor antigen p53 (Tumor suppressor p53).  
GN Name:P53;  
OS Cercopithecus aethiops (Green monkey) (Grivet).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecidae; Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Liver;  
RX MEDLINE=90045967; PubMed=2530498;  
RA Rigaudy P., Eckhardt W.;  
RT "Nucleotide sequence of a cDNA encoding the monkey cellular  
RT phosphoprotein p53.";  
RL Nucleic Acids Res. 17:8375-8375(1989).  
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
CC growth arrest or apoptosis depending on the physiological  
CC circumstances and cell type. Involved in cell cycle regulation as  
CC a trans-activator that acts to negatively regulate cell division  
CC by controlling a set of genes required for this process. One of  
CC the activated genes is an inhibitor of cyclin-dependent kinases.  
CC Apoptosis induction seems to be mediated either by stimulation of  
CC BAX and FAS antigen expression, or by repression of Bcl-2  
CC expression.  
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC -1- SUBUNIT: Binds DNA as a homotrimer. Found in a complex with  
CC CABE1 and p53/TP73. Interacts with histone acetyltransferases  
CC EP300 and methyltransferases HR23L and CARM1, and recruits them  
CC to promoters. C-terminus interacts with TAF1, when TAF1 is part of  
CC the TFIID complex. Interacts with HIPK1, HIPK2, AXIN1, and  
CC p53DINP1. Part of a complex consisting of TP53, HIPK2 and AXIN1.  
CC Interacts with WWOX (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).  
CC -1- PTM: Phosphorylated. Phosphorylation on Ser residues mediates  
CC transcriptional activation. Phosphorylated on Thr-18 by VRK1,  
CC which may prevent the interaction with MDM2. Phosphorylated on  
CC Thr-55 by TAF1 which promotes MDM2-mediated p53 degradation.  
CC Phosphorylated by HIPK1. Phosphorylated on Ser-46 by HIPK2 upon UV  
CC irradiation. Phosphorylation on Ser-46 is required for acetylation  
CC by CREBBP (By similarity).  
CC -1- PTM: Acetylated. Its deacetylation by SIRT1 impairs its ability to  
CC induce proapoptotic program and modulate cell senescence (By  
CC similarity).  
CC -1- DISEASE: p53 is found in increased amounts in a wide variety of  
CC transformed cells. p53 is frequently mutated or inactivated in  
CC many types of cancer.  
CC -1- SIMILARITY: Belongs to the p53 family.  
CC  
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CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC  
CC EMBL: X16384; CAJ34420.1; -; mRNA.  
CC F1R; S06594; S06594.  
CC HSSP; P04637; 10LG.  
CC SMR; P13481; 94-289.  
CC GO; GO:0005739; C:mitochondrion; ISS.

DR GO; GO:0005730; C:nucleolus; ISS.  
DR GO; GO:0005524; F:ATP binding; ISS.  
DR GO; GO:0005507; F:copper ion binding; ISS.  
DR GO; GO:0003677; F:DNA binding; ISS.  
DR GO; GO:0000739; F:DNA strand annealing activity; ISS.  
DR GO; GO:0005515; F:protein binding; ISS.  
DR GO; GO:0006915; F:apoptosis; ISS.  
DR GO; GO:0006284; F:base-excision repair; ISS.  
DR GO; GO:0008635; F:caseinase activation via cytochrome c; ISS.  
DR GO; GO:0007569; P:cell aging; ISS.  
DR GO; GO:0007050; P:cell cycle arrest; ISS.  
DR GO; GO:0030154; P:cell differentiation; ISS.  
DR GO; GO:0008283; P:cell proliferation; ISS.  
DR GO; GO:0030308; P:negative regulation of cell growth; ISS.  
DR GO; GO:0006289; P:nucleotide-excision repair; ISS.  
DR InterPro; IPR002117; P53.  
DR InterPro; IPR011615; P53\_DNA\_bd.  
DR InterPro; IPR012346; P53\_RUNT\_DNA\_bd.  
DR InterPro; IPR010991; P53\_tetramer1stn.  
DR Pfam; PF007710; P53\_tetramer; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR PRODOM; PD002681; P53; 1.  
DR PROSITE; PS00348; P53; 1.  
KM Acetylation; Activator; Anti-oncogene; Apoptosis; Cell cycle;  
KM DNA-binding; Metal-binding; Nuclear protein; Phosphorylation;  
KM Transcription; Transcription regulation; Zinc.  
FT CHAIN 1 393  
FT DNA BIND 102 292  
FT REGION 1 83  
FT REGION 1 44  
FT REGION 66 110  
FT REGION 100 370  
FT REGION 116 292  
FT REGION 310 393  
FT REGION 319 360  
FT REGION 325 356  
FT REGION 368 387  
FT MOTIF 305 321  
FT MOTIF 339 350  
FT METAL 176 176  
FT METAL 179 179  
FT METAL 238 238  
FT METAL 242 242  
FT BINDING 392 392  
FT MOD\_RES 15 15  
FT MOD\_RES 18 18  
FT MOD\_RES 46 46  
FT MOD\_RES 55 55  
FT MOD\_RES 305 305  
FT MOD\_RES 373 373  
FT MOD\_RES 382 382  
SQ SEQUENCE 393 AA; 43696 MW; 9ED285CA785506E CRC64;  
Query Match 94.3%; Score 99; DB 1; Length 393;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 PPLSQTFSIDLWKLLEN 18  
12 PPLSQTFSIDLWKLLEN 29

Db

RESULT 9  
P53\_HUMAN STANDARD; PRT; 393 AA.  
ID P53\_HUMAN  
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AC Q16810; Q16811; Q16848; Q80016; Q99659; Q9BTM4; Q9HA08;

AC O9NP68; O9NP42; O9NZD0; O9UB12; O9U061;  
 DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JUL-1989, Sequence version 2.  
 DT 07-MAR-2006, entry version 101.  
 DE Cellular tumor antigen p53 (Tumor suppressor p53) (Phosphoprotein p53)  
 DE (Antigen NY-CO-13).  
 GN Name:TP53; Synonyms=p53;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=85230577; PubMed=4006916;  
 RA Zakut-Houri R., Blenz-Radmer B., Girol D., Oren M.;  
 RT "Human p53 cellular tumor antigen: cDNA sequence and expression in COS  
 RT cells.";  
 RL EMOB J. 4:1251-1255(1985).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=87064416; PubMed=2946935;  
 RA Lamb P., Crawford L.;  
 RT "Characterization of the human p53 gene.";  
 RL Mol. Cell. Biol. 6:1379-1385(1986).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=85267676; PubMed=3894933;  
 RA Harlow E., Williamson N.M., Ralston R., Helfman D.M., Adams T.E.;  
 RT "Molecular cloning and in vitro expression of a cDNA clone for human  
 RT cellular tumor antigen p53.";  
 RL Mol. Cell. Biol. 5:1601-1610(1985).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=87089826; PubMed=3025664;  
 RA Harris N., Brill E., Shohat O., Prokocimer M., Wolf D., Aral N.,  
 RA Rotter V.;  
 RT "Molecular basis for heterogeneity of the human p53 protein.";  
 RL Mol. Cell. Biol. 6:4650-4656(1986).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=89108008; PubMed=2905688; DOI=10.1016/0378-1119(88)90196-5;  
 RA Buchann V.L., Chumakov P.M., Ninkina N.N., Samarina O.P.,  
 RA Georgiev G.P.;  
 RT "A variation in the structure of the protein-coding region of the  
 RT human p53 gene.";  
 RL Gene 70:245-252(1988).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE OF 101-393.  
 RX MEDLINE=85126934; PubMed=6396087;  
 RA Matlashewski G., Lamb P., Pim D., Peacock J., Crawford L.,  
 RA Benichou S.;  
 RT "Isolation and characterization of a human p53 cDNA clone: expression  
 RT of the human p53 gene.";  
 RL EMOB J. 3:3257-3262(1984).  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE, VARIANTS BURKITT'S LYMPHOMA, AND VARIANT ARG-72.  
 RX MEDLINE=92007731; PubMed=1915267;  
 RA Faircl P.J., Allen G., Shanahan F., Vousden K.H., Crook T.;  
 RT "p53 is frequently mutated in Burkitt's lymphoma cell lines.";  
 RL EMOB J. 10:2879-2887(1991).  
 RN [8]  
 RP NUCLEOTIDE SEQUENCE, AND VARIANTS ARG-72 AND LYS-286.  
 RX MEDLINE=93303270; PubMed=8316628;  
 RA Allalunis-Turner M.J., Barton G.M., Day R.S. III, Dobler K.D.,  
 RA Mirzayans R.;  
 RT "Isolation of two cell lines from a human malignant glioma specimen  
 RT differing in sensitivity to radiation and chemotherapeutic drugs.";  
 RL Radiat. Res. 134:349-354(1993).  
 RN [9]  
 RP NUCLEOTIDE SEQUENCE, VARIANT ARG-72, AND INTERACTION WITH WMOX.  
 RX MEDLINE=21264809; PubMed=11058590; DOI=10.1074/jbc.M007140200;  
 RA Chang N.-S., Pratt N., Heath J., Schultz L., Slave D., Carey G.B.,  
 RA Zevotek N.;  
 RT "Hydrolidase induction of a WMOX domain-containing oxidoreductase that  
 RT enhances tumor necrosis factor cytotoxicity.";  
 RL J. Biol. Chem. 276:3361-3370(2001).  
 RN [10]  
 RP NUCLEOTIDE SEQUENCE.  
 RX Chumakov P.M., Almazov V.P., Jenkins J.R.;  
 RT Submitted (JUN-1991) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP NUCLEOTIDE SEQUENCE.  
 RX Rosemuller E.H., Tilanus M.G.J.;  
 RT "p53 genomic sequence. Corrections and polymorphism.";  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP NUCLEOTIDE SEQUENCE, AND VARIANTS SER-47; ARG-72; LYS-339 AND ALA-366.  
 RX Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,  
 RA Nguyen C.P., Gilderleeve H., Cassidy C.M., Johnson E.J.,  
 RA Swanson J.E., McFarland I., Yool B., Park C., Nickerson D.A.;  
 RT "NIHES-SNP8, environmental genome project, NIHES ES15478, Department  
 RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";  
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
 RN [13]  
 RP NUCLEOTIDE SEQUENCE, AND VARIANTS ARG-72 AND LYS-286.  
 RX PubMed=11023613;  
 RA Anderson C.W., Allalunis-Turner M.J.;  
 RT "Human TP53 from the malignant glioma-derived cell lines M059J and  
 RT M059K has a cancer-associated mutation in exon 8.";  
 RL Radiat. Res. 154:473-476(2000).  
 RN [14]  
 RP NUCLEOTIDE SEQUENCE, AND VARIANTS ARG-72; HIS-273 AND SER-309.  
 RA Aruma K., Shichijo S., Itoh K.;  
 RT "Identification of a tumor-rejection antigen recognized by HLA-B\*46  
 RT restricted CTL.";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [15]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA), AND VARIANTS ARG-72 AND  
 RP ALA-278  
 RC TTSDB=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettlemen M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilg D.E.,  
 RA Schenck A., Schein J.E., Jones S.J.M., Maita W.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [16]  
 RP NUCLEOTIDE SEQUENCE OF 1-379, AND VARIANTS ARG-72 AND ASN-139.  
 RC TTSDB=Lung carcinoma;  
 RX PubMed=14660794; DOI=10.1073/pnas.2536558100;  
 RA Kanashiro C.A., Schally A.V., Grook K., Armatis P., Bernardino A.L.,  
 RA Varga J.L.;  
 RT "Inhibition of mutant p53 expression and growth of DMS-153 small cell  
 RT lung carcinoma by antagonists of growth hormone-releasing hormone and  
 RT bombesin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15836-15841(2003).  
 RN [17]  
 RP NUCLEOTIDE SEQUENCE OF 126-185.  
 RX Pan X.L., Zhang A.H.;  
 RT "Study on the effect of tumor suppressor gene p53 in arsenism

RT Patients.";  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
RN [18]  
RP NUCLEOTIDE SEQUENCE OF 261-298.  
RC TISSUE=Blood;  
RA Nimri L.F., Owais W., Momani E.;  
RT "Detection of p53 gene mutations and serum p53 antibodies associated  
RT with cigarette smoking.";  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
RN [19]  
RP NUCLEOTIDE SEQUENCE OF 262-306.  
RC TISSUE=Ovarian adenocarcinoma;  
RA Filippini G., Soldati G.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
RN [20]  
RP NUCLEOTIDE SEQUENCE OF 225-260.  
RC TISSUE=Gial cell, and Gial tumor;  
RA Thompson-Hehr J., Davies M.P.A., Green J.A., Halliwell N.,  
RA Joyce K.A., Salisbury J., Sibson D.R., Vergote I., Walker C.;  
RT "Mutation detection utilizing a novel PCR approach for amplification  
RT of the p53 gene from microdissected tissue: application to archival  
RT tumor samples.";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [21]  
RP NUCLEOTIDE SEQUENCE OF 225-260.  
RA Yavuz A.S., Farmer N.L., Yavuz S., Grammer A.C., Gitschick H.J.,  
RA Lipkay P.E.;  
RT "Bcl-2 and p53 gene mutations in consillar B cells.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [22]  
RP NUCLEOTIDE SEQUENCE OF 332-366.  
RA Pinto E.M., Mendonca B.B., Latronico A.C.;  
RT "Allelic variant in intron 9 of TP53 gene";  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
RN [23]  
RP RNA-BINDING.  
RX MEDLINE=91141509; PubMed=1705009;  
RA Samad A., Carroll R.B.;  
RT "The tumor suppressor p53 is bound to RNA by a stable covalent  
RT linkage.";  
RL Mol. Cell. Biol. 11:1598-1606(1991).  
RN [24]  
RP ALTERNATIVE SPLICING.  
RX MEDLINE=96197761; PubMed=8632903;  
RA Plamen J.-M., Maridel F., Estreicher A., Vannier A., Lmacher J.-M.,  
RA Gilbert D., Iggo R., Frebourg T.;  
RT "The human tumour suppressor gene p53 is alternatively spliced in  
RT normal cells.";  
RL Oncogene 12:813-818(1996).  
RN [25]  
RP NUCLEAR LOCALIZATION SIGNAL.

Query Match 94.3%; Score 99; DB 1; Length 393;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSOETFSIDLMLPEN 18  
Db 12 PPLSOETFSIDLMLPEN 29

RESULT 10  
P53\_MACFA STANDARD; PRT; 393 AA.  
AC P56423;  
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.  
DT 10-MAY-2004, sequence version 2.  
DT 07-FEB-2006, entry version 50.  
DE Cellular tumor antigen p53 (tumor suppressor p53).  
GN Name=TP53; Synonyms=p53;  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

OC Cercopithecidae; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RA Khan M.A., Hansen C., Welsh J.A., Bennett W.P.;  
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=skin;  
RX MEDLINE=22094611; PubMed=12099687; DOI=10.1016/S0006-291X(02)00730-1;  
RA Shimizu Y., Ishida T.;  
RT "Somatic mutations in the p53 gene account for the extension of  
RT replicative life span of macaque cells.";  
RL Biochem. Biophys. Res. Commun. 295:644-650(2002).  
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
CC growth arrest or apoptosis depending on the physiological  
CC circumstances and cell type. Involved in cell cycle regulation as  
CC a trans-activator that acts to negatively regulate cell division  
CC by controlling a set of genes required for this process. One of  
CC the activated genes is an inhibitor of cyclin-dependent kinases.  
CC Apoptosis induction seems to be mediated either by stimulation of  
CC BAX and FAS antigen expression, or by repression of Bcl-2  
CC expression.  
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC -1- SUBUNIT: Binds DNA as a homotetramer. Found in a complex with  
CC CABP1 and p53/TP73. Interacts with histone acetyltransferases  
CC EP300 and methyltransferases HR23A and CBML, and recruits them  
CC to promoters. C-terminus interacts with TAP1, when TAP1 is part of  
CC the TRFID complex. Interacts with H1PK1, H1PK2, AXIN1, and  
CC P53DINP1. P53DINP1. Part of a complex consisting of TP53, H1PK2  
CC and AXIN1. Interacts with WMOX (By similarity).  
CC SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).  
CC -1- PTM: Acetylated. Its deacetylation by SIRT1 impairs its ability to  
CC induce proapoptotic program and modulate cell senescence (By  
CC similarity).  
CC -1- PTM: Phosphorylated. Phosphorylation on Ser residues mediates  
CC transcriptional activation. Phosphorylated on Thr-18 by VRK1,  
CC which may prevent the interaction with MDM2. Phosphorylated on  
CC Thr-55 by TAP1 which promotes MDM2-mediated p53 degradation.  
CC Phosphorylated by H1PK1. Phosphorylated on Ser-46 by H1PK2 upon UV  
CC irradiation. Phosphorylation on Ser-46 is required for acetylation  
CC by CREBBP (By similarity).  
CC -1- DISEASE: p53 is found in increased amounts in a wide variety of  
CC transformed cells. p53 is frequently mutated or inactivated in  
CC many types of cancer.  
CC -1- SIMILARITY: Belongs to the p53 family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivs license  
CC -----  
DR EMBL: U48957; AAB91535.1; -; Genomic DNA.  
DR EMBL: AF456343; AAN64027.1; -; mRNA.  
DR HSSP: P04637; 10L6.  
DR SMR: P56423; 94-289.  
DR GO: GO:0005739; C:nucleochondrion; ISS.  
DR GO: GO:0005730; C:nucleolus; ISS.  
DR GO: GO:0005524; F:ATP binding; ISS.  
DR GO: GO:0005507; F:copper ion binding; ISS.  
DR GO: GO:0003677; F:DNA binding; ISS.  
DR GO: GO:0007039; F:DNA strand annealing activity; ISS.  
DR GO: GO:0005515; F:protein binding; ISS.  
DR GO: GO:0006915; F:apoptosis; ISS.  
DR GO: GO:0006284; P:base-excision repair; ISS.  
DR GO: GO:0006935; P:caspace activation via cytochrome c; ISS.  
DR GO: GO:0007569; P:cell aging; ISS.  
DR GO: GO:0007050; P:cell cycle arrest; ISS.  
DR GO: GO:00030154; P:cell differentiation; ISS.  
DR GO: GO:0008283; P:cell proliferation; ISS.  
DR GO: GO:0003008; P:negative regulation of cell growth; ISS.  
DR GO: GO:0006289; P:nucleotide-excision repair; ISS.  
DR InterPro: IPR002117; P53.  
DR InterPro: IPR011615; P53\_DNA\_bd.  
DR InterPro: IPR012346; P53\_RUNT\_DNA\_bd.

DR InterPro: IPR010991; p53\_tetrameriscn.  
DR Pfam: PF00870; p53\_1.  
DR PRINTS: PR007710; p53\_tetramer; 1.  
DR PRODOM: PD002681; p53; 1.  
DR PROSITE: PS00348; p53; 1.  
KM Acetylation: Acetylator; Anti-oncogene; Apoptosis; Cell cycle;  
KM DNA-binding; Metal-binding; Nuclear protein; Phosphorylation;  
KM Transcription; Transcription regulation; Zinc.  
FT CHAIN 1 393  
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FT DNA BIND 102 292  
FT REGION 1 83  
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FT REGION 66 110  
FT REGION 100 370  
FT REGION 116 292  
FT REGION 300 393  
FT REGION 319 360  
FT REGION 325 356  
FT REGION 368 387  
FT MOTIF 305 321  
FT MOTIF 339 350  
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FT METAL 179 179  
FT METAL 238 238  
FT METAL 242 242  
FT BINDING 392 392  
FT FT  
FT MOD\_RES 15 15  
FT MOD\_RES 18 18  
FT MOD\_RES 46 46  
FT MOD\_RES 55 55  
FT MOD\_RES 305 305  
FT MOD\_RES 373 373  
FT MOD\_RES 382 382  
FT CONFLICT 30 30  
SQ SEQUENCE 393 AA; 43655 MW; E212E54FE650103 CRC64;  
Query Match 94.3%; Score 99; DB 1; Length 393;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPSQETFSDLWKLPEN 18  
Db 12 PPSQETFSDLWKLPEN 29  
RESULT 11  
P53\_MACFU STANDARD; PRT; 393 AA.  
AC P61260;  
DT 10-MAY-2004, integrated into UniProtKB/Swiss-Prot.  
DT 10-MAY-2004, sequence version 1.  
DT 07-FEB-2006, entry version 25.  
DE Cellular tumor antigen p53 (tumor suppressor p53).  
GN Name:TP53; Synonyms:p53;  
OS Macaca fuscata fuscata (Japanese macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecoidea; Cercopithecinae; Macaca.  
OX NCBI\_Taxid=9543;  
RN 1  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=lung.  
RX MEDLINE=22094611; PubMed=12099687; DOI=10.1016/S0006-291X(02)00730-1;  
RA Shimizu Y., Ishida T.,  
RT "Somatic mutations in the p53 gene account for the extension of  
RT replicative life span of macaque cells.";  
RL Biochem. Biophys. Res. Commun. 295:644-650(2002).

CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
CC growth arrest or apoptosis depending on the physiological  
CC circumstances and cell type. Involved in cell cycle regulation as  
CC a trans-activator that acts to negatively regulate cell division  
CC by controlling a set of genes required for this process. One of  
CC the activated genes is an inhibitor of cyclin-dependent kinases.  
CC Apoptosis induction seems to be mediated either by stimulation of  
CC BAX and FAS antigen expression, or by repression of Bcl-2  
CC expression.  
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity). Found in a  
CC complex with CABP1 and p53/TP73 (By similarity). Interacts with  
CC histone acetyltransferases EP300 and methyltransferases HMT112  
CC and CARM1, and recruits them to promoters. Interacts with WMOX (By  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).  
CC -1- PTM: Phosphorylated on Thr-18 by VRK1, which may prevent the  
CC interaction with MDM2 (By similarity).  
CC -1- PTM: Acetylated. Its deacetylation by SIRT1 impairs its ability to  
CC induce proapoptotic program and modulate cell senescence (By  
CC similarity).  
CC -1- PTM: Phosphorylated on Thr-55 by TAF1 which promotes MDM2-mediated  
CC p53 degradation (By similarity).  
CC -1- DISEASE: p53 is found in increased amounts in a wide variety of  
CC transformed cells. p53 is frequently mutated or inactivated in  
CC many types of cancer.  
CC -1- SIMILARITY: Belongs to the p53 family.  
CC  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonCommercial License  
CC  
CC EMBL: AF456344; AA064028.1; -; mRNA.  
CC SMR: P61260; 94-289.  
CC DR GO: GO:0005739; C:mitochondrion; ISS.  
CC DR GO: GO:0005730; C:nucleolus; ISS.  
CC DR GO: GO:0005524; F:ATP binding; ISS.  
CC DR GO: GO:0005507; F:copper ion binding; ISS.  
CC DR GO: GO:0003677; F:DNA binding; ISS.  
CC DR GO: GO:0000739; F:DNA strand annealing activity; ISS.  
CC DR GO: GO:0005515; F:protein binding; ISS.  
CC DR GO: GO:0006915; F:apoptosis; ISS.  
CC DR GO: GO:0006284; P:base-excision repair; ISS.  
CC DR GO: GO:000635; P:casepase activation via cytochrome c; ISS.  
CC DR GO: GO:0007569; P:cell aging; ISS.  
CC DR GO: GO:0007050; P:cell cycle arrest; ISS.  
CC DR GO: GO:0030154; P:cell differentiation; ISS.  
CC DR GO: GO:0008283; P:cell proliferation; ISS.  
CC DR GO: GO:0030308; P:negative regulation of cell growth; ISS.  
CC DR GO: GO:0006289; P:nucleotide-excision repair; ISS.  
CC DR InterPro: IPR002117; p53.  
CC DR InterPro: IPR011615; p53\_DNA\_bd.  
CC DR InterPro: IPR012346; p53\_RUNT\_DNA\_bd.  
CC DR InterPro: IPR010991; p53\_tetrameriscn.  
CC DR Pfam: PF00870; p53\_1.  
CC DR Pfam: PF007710; p53\_tetramer; 1.  
CC DR PRINTS: PR00386; P53SUPPRESSR.  
CC DR PRODOM: PD002681; p53; 1.  
CC DR PROSITE: PS00348; p53; 1.  
CC KM Acetylation: Acetylator; Anti-oncogene; Apoptosis; Cell cycle;  
CC KM DNA-binding; Metal-binding; Nuclear protein; Phosphorylation;  
CC Transcription; Transcription regulation; Zinc.  
FT CHAIN 1 393  
/Pfam-PRO 0000185705.  
FT DNA BIND 102 292  
FT REGION 1 83  
FT REGION 1 44  
FT REGION 66 110  
FT REGION 100 393  
FT REGION 300 393  
FT REGION 325 356  
FT REGION 368 387  
FT MOTIF 305 321  
FT MOTIF 339 350  
Nuclear export signal (By similarity).

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FT METAL 176 176 zinc (By similarity).
FT METAL 179 179 zinc (By similarity).
FT METAL 238 238 zinc (By similarity).
FT METAL 242 242 zinc (By similarity).
FT BINDING 392 392 5'-phospho-RNA (covalent) (By
FT similarity).
FT MOD_RES 15 15 phosphoserine (by PRPK) (By similarity).
FT MOD_RES 18 18 phosphothreonine (by VRK1) (By
FT similarity).
FT MOD_RES 55 55 phosphothreonine (by TAF1) (By
FT similarity).
FT MOD_RES 305 305 N6-acetyllysine (By similarity).
FT MOD_RES 373 373 N6-acetyllysine (By similarity).
FT MOD_RES 382 382 N6-acetyllysine (By similarity).
SQ SEQUENCE 393 AA; 43655 MW; E212E5E4FE650103 CRC64;

Query Match 94.3%; Score 99; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQTFSDDLWKLLEN 18
Db 12 PPLSQTFSDDLWKLLEN 29

RESULT 12
P53_MACMU STANDARD; PRT; 393 AA.
ID P53_MACMU
AC P56424;
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 15-JUL-1998, sequence version 1.
DI 07-FEB-2006, entry version 50.
DE Cellular tumor antigen p53 (Tumor suppressor p53).
OS Name=TP53; Synonyms=p53;
Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Blood;
RA MEDLINE=94171042; Pubmed=8125305; DOI=10.1016/0378-1119(94)90812-5;
RX Kay H.D., Mountjoy C.P., Wu G., Cornish K.G., Smith L.J.;
RT "Sequence of a cDNA encoding the p53 protein in rhesus monkey (Macaca
mulatta).";
RL Gene 138:223-226 (1994).
RN [2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Khan M.A., Hansen C., Welsh J.A., Bennett W.P.;
RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Binds DNA as a homotetramer. Found in a complex with
CC CABP1 and p53/TP73. Interacts with histone acetyltransferases
CC EP300 and methyltransferases HMT1L2 and CARM1, and recruits them
CC to promoters. C-terminus interacts with TAF1, when TAF1 is part of
CC the TFIID complex. Interacts with HIPK1, HIPK2, AXIN1, and
CC p53INP1. Part of a complex consisting of TP53, HIPK2 and AXIN1.
CC Interacts with WWOX (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -!- PTM: Acetylated. Its deacetylation by SIRT1 impairs its ability to
CC induce proapoptotic program and modulate cell senescence (By
CC similarity).
CC -!- PTM: Phosphorylated. Phosphorylation on Ser residues mediates
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```
CC transcriptional activation. Phosphorylated on Thr-18 by VRK1,
CC which may prevent the interaction with MDM2. Phosphorylated on
CC Thr-55 by TAF1 which promotes MDM2-mediated p53 degradation.
CC Phosphorylated by HIPK1. Phosphorylated on Ser-46 by HIPK2 upon UV
CC irradiation. Phosphorylation on Ser-46 is required for acetylation
CC by CREBBP (By similarity).
CC -!- DISEASE: p53 is found in increased amounts in a wide variety of
CC transformed cells. p53 is frequently mutated or inactivated in
CC many types of cancer.
CC -!- SIMILARITY: Belongs to the p53 family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonCommercial license
CC
CC EMBL: L20442; AAA17994.1; -; mRNA.
CC EMBL: U48956; AAB81534.1; -; Genomic DNA.
CC HSSP: P04637; 10LG.
CC SMR: P56424; 94-289.
CC GO: GO:0005739; C:mitochondrion; ISS.
CC GO: GO:0005730; C:nucleolus; ISS.
CC GO: GO:0005524; F:AMP binding; ISS.
CC GO: GO:0005507; F:copper ion binding; ISS.
CC GO: GO:0003677; F:DNA binding; ISS.
CC GO: GO:0000739; F:DNA strand annealing activity; ISS.
CC GO: GO:0005515; F:protein binding; ISS.
CC GO: GO:0006915; F:apoptosis; ISS.
CC GO: GO:0006284; F:base-excision repair; ISS.
CC GO: GO:0008635; F:casease activation via cytochrome c; ISS.
CC GO: GO:0007569; P:cell aging; ISS.
CC GO: GO:0007050; P:cell cycle arrest; ISS.
CC GO: GO:0030154; P:cell differentiation; ISS.
CC GO: GO:0008283; P:cell proliferation; ISS.
CC GO: GO:0030308; P:negative regulation of cell growth; ISS.
CC GO: GO:0006289; P:nucleotide-excision repair; ISS.
CC InterPro: IPR002117; P53.
CC InterPro: IPR011615; P53 DNA_bd.
CC InterPro: IPR012346; P53 RUND DNA_bd.
CC InterPro: IPR010991; P53_tetramer1stn.
CC Pfam: PR00870; P53; 1.
CC Pfam: PR07710; P53_tetramer; 1.
CC PRINTS: PR00386; P53SUPPRESSR.
CC ProDom: PD002681; P53; 1.
CC PROSITE: PS00348; P53; 1.
CC Acetylation: Activator; Anti-oncogene; Apoptosis; Cell cycle;
CC DNA-binding; Metal-binding; Nuclear protein; Phosphorylation;
CC Transcription; Transcription regulation; Zinc.
CC CHAIN 1 393
FT DNA BIND 102 232
FT REGION 1 83
FT REGION 1 44
FT REGION 66 110
FT REGION 100 370
FT REGION 116 292
FT REGION 300 333
FT REGION 319 360
FT REGION 325 356
FT REGION 368 387
FT MOTIF 305 321
FT MOTIF 339 350
FT METAL 176 176 zinc (By similarity).
FT METAL 179 179 zinc (By similarity).
FT METAL 238 238 zinc (By similarity).
FT METAL 242 242 zinc (By similarity).
FT BINDING 392 392 5'-phospho-RNA (covalent) (By
FT similarity).
FT MOD_RES 15 15 phosphoserine (by PRPK) (By similarity).
FT MOD_RES 18 18 phosphothreonine (by VRK1) (By
FT similarity).
FT MOD_RES 46 46 phosphoserine (by HIPK2) (By similarity).
FT MOD_RES 55 55 phosphothreonine (by TAF1) (By
FT similarity).
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FT MOD_RES 305 305 N6-acetyllysine (By similarity).
FT MOD_RES 373 373 N6-acetyllysine (By similarity).
FT MOD_RES 382 382 N6-acetyllysine (By similarity).
SQ SEQUENCE 393 AA; 43555 MW; E212E54FE550103 CRC64;

Query Match 94.3%; Score 99; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQTFSDLWKLPEN 18
12 PPLSQTFSDLWKLPEN 29

RESULT 13
P53_TUPGB STANDARD; PRT; 393 AA.
ID P53_TUPGB
AC O9TAL1;
DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 50.
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN Name=P53; Synonyms=P53;
OS Tupaiia glis belangeri (Common tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupaiia.
OC NCB1_TaxId=37347;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Chinensis; TISSUE=Liver;
RA Park U., Lee Y.;
RT "Wild-type p53 sequence of tree shrews.";
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Binds DNA as a homotrimer. Interacts with histone
CC acetyltransferases EP300 and methyltransferases HR23LT12 and CARM1,
CC and recruits them to promoters. C-terminus interacts with TAF1,
CC when TAF1 is part of the TFIID complex. Interacts with HIPK1,
CC HIPK2, AXIN1, and P53DINP1. Part of a complex consisting of TP53,
CC HIPK2 and AXIN1. Interacts with WWOX (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -!- PTM: Acetylated. Its deacetylation by SIRT1 impairs its ability to
CC induce proapoptotic program and modulate cell senescence (By
CC similarity).
CC -!- PTM: Phosphorylated. Phosphorylation on Ser residues mediates
CC transcriptional activation. Phosphorylated on Thr-18 by VRK1,
CC which may prevent the interaction with MDM2. Phosphorylated on
CC Thr-55 by TAF1 which promotes MDM2-mediated p53 degradation.
CC Phosphorylated by HIPK1 (By similarity). Phosphorylation on Ser-46
CC by HIPK2 upon UV irradiation. Phosphorylation on Ser-46 is
CC required for acetylation by CREBBP (By similarity).
CC -!- DISEASE: p53 is found in increased amounts in a wide variety of
CC transformed cells. p53 is frequently mutated or inactivated in
CC many types of cancer.
CC -!- SIMILARITY: Belongs to the p53 family.
CC
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CC
DR EMBL, A0175893; AAP22640.1; -. mRNA.
DR HSSP, P04637; IGZ8.
DR SMR, O9TAL1; 94-289.
DR GO, GO:0005739; C:nucleolus; ISS.
DR GO, GO:0005730; C:nucleolus; ISS.

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DR GO, GO:0005524; F:ATP binding; ISS.
DR GO, GO:0005507; F:copper ion binding; ISS.
DR GO, GO:0003677; F:DNA binding; ISS.
DR GO, GO:0000739; F:DNA strand annealing activity; ISS.
DR GO, GO:0005515; F:protein binding; ISS.
DR GO, GO:0006915; F:apoptosis; ISS.
DR GO, GO:0006284; F:base-excision repair; ISS.
DR GO, GO:0006355; F:caspace activation via cytochrome c; ISS.
DR GO, GO:0007659; P:cell aging; ISS.
DR GO, GO:0007050; P:cell cycle arrest; ISS.
DR GO, GO:0030154; P:cell differentiation; ISS.
DR GO, GO:0008283; P:cell proliferation; ISS.
DR GO, GO:0030308; P:negative regulation of cell growth; ISS.
DR GO, GO:0006289; P:nucleotide-excision repair; ISS.
DR InterPro, IPR002117; P53.
DR InterPro, IPR011615; P53_DNA_bd.
DR InterPro, IPR012346; P53_RUNT_DNA_bd.
DR InterPro, IPR010991; P53_tetramerictn.
DR Pfam, PF006870; P53_1.
DR Pfam, PF07710; P53_tetramer; 1.
DR PRINTS, PR00386; P53SUPPRESSR.
DR PRODOM, PD002681; P53; 1.
DR PROSITE, PS00348; P53; 1.
KW Acetylation; Activator; Anti-oncogene; Apoptosis; Cell cycle;
KW DNA-binding; Metal-binding; Nuclear protein; Phosphorylation;
KW Transcription; Transcription regulation; Zinc.
FT CHAIN 1
FT FT
FT DNA BIND 102 292
FT REGION 1 83
FT REGION 1 44
FT REGION 66 110
FT REGION 100 370
FT REGION 116 292
FT REGION 300 393
FT REGION 319 360
FT REGION 325 355
FT REGION 368 387
FT MOTIF 305 321
FT MOTIF 339 350
FT METAL 176 176
FT METAL 179 179
FT METAL 238 238
FT METAL 242 242
FT BINDING 392 392
FT MOD_RES 15 15
FT MOD_RES 18 18
FT MOD_RES 46 46
FT MOD_RES 55 55
FT MOD_RES 305 305
FT MOD_RES 373 373
FT MOD_RES 382 382
SQ SEQUENCE 393 AA; 43552 MW; FD936003945A1FA CRC64;

Query Match 94.3%; Score 99; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQTFSDLWKLPEN 18
12 PPLSQTFSDLWKLPEN 29

RESULT 14
Q50UE4_HUMAN PRELIMINARY; PRT; 393 AA.
ID Q50UE4_HUMAN
AC Q50UE4;
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 1.

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DT 07-FEB-2006, entry version 10.
DE Tumor protein p53 (Li-Fraumeni syndrome).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koudinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDS in BD Creator(TM) System Donor
RT vector."
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
CC
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CC
EMBL: BT019622; AAV38428.1; -; mRNA.
DR SMR; Q5U0E4; 94-289.
DR Ensembl; ENSG00000141510; Homo sapiens.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; P:metal ion binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0007049; P:cell cycle; IEA.
DR GO; GO:0045786; P:negative regulation of progression through . . .; IEA.
DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR002117; P53.
DR InterPro; IPR011615; P53_DNA_bd.
DR InterPro; IPR012346; P53_RUNT_DNA_bd.
DR InterPro; IPR010991; P53_tetramerisn.
DR Pfam; PF00870; P53_1.
DR Pfam; PF07710; P53_tetramer; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Activator; Anti-oncogene; Apoptosis; Cell cycle; DNA-binding;
KW Metal-binding; Nuclear protein; Phosphorylation; Transcription;
KW Transcription regulation; Zinc.
SQ SEQUENCE 393 AA; 43730 MW; 6610C5F3491C530E CRC64;

Query Match 94.3%; Score 99; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETPSDLWKLPEN 18
DB 12 PPLSQETPSDLWKLPEN 29

```

```

RESULT 15
Q2XN98 HUMAN
ID Q2XN98_HUMAN PRELIMINARY; PRT; 393 AA.
AC Q2XN98;
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE P53 protein.
GN Name=P53;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Normal colon;
RX PubMed=16131611; DOI=10.1101/Gad.1339905;
RA Bourdon J.C., Fernandes K., Murray-Zmijewski F., Liu G., Diot A.,

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RA Xirodimas D.P., Saville M.K., Lane D.P.;
RT "p53 isoforms can regulate p53 transcriptional activity.";
RL Genes Dev. 19:2122-2137(2005).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC
EMBL: DQ286964; ABB80266.1; -; mRNA.
DR EMBL; DQ191317; ABB80262.1; -; mRNA.
KW Activator; Anti-oncogene; Apoptosis; Cell cycle; DNA-binding;
KW Metal-binding; Nuclear protein; Phosphorylation; Transcription;
KW Transcription regulation; Zinc.
SQ SEQUENCE 393 AA; 43712 MW; AC611E4938C7BC3B CRC64;

Query Match 94.3%; Score 99; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETPSDLWKLPEN 18
DB 12 PPLSQETPSDLWKLPEN 29

```

Search completed: July 5, 2006, 22:45:46  
Job time : 296 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 22:37:11 ; Search time 196 Seconds  
(without alignments)  
44.322 Million cell updates/sec

Title: US-09-403-440A-2  
Perfect score: 105  
Sequence: 1 PPLSQETFSDFMLKLPENG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*
- 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	19	AAW82321	Aaw82321 p53 homol
2	105	100.0	19	AAW82319	Aaw82319 p53 homol
3	99	94.3	18	AAW37228	Aaw37228 p53 N-ter
4	99	94.3	20	AAE30863	Aae30863 EGFP-BOX-
5	99	94.3	25	AAE54907	Aae54907 Immunodom
6	99	94.3	25	AAE51879	Aae51879 Human p53
7	99	94.3	26	AAW60202	Aaw60202 p53 pep1
8	99	94.3	32	AAE30523	Aab30523 Peptide f
9	99	94.3	32	ADJ25788	Adj25788 MDM2 bind
10	99	94.3	32	ADZ48535	Adz48535 Human p53
11	99	94.3	36	AAW13604	Aaw13604 p53 prote
12	99	94.3	41	AAW13603	Aaw13603 p53 prote
13	99	94.3	50	ADT02859	Adt02859 Human p53
14	99	94.3	52	AAW13602	Aaw13602 p53 prote
15	99	94.3	64	AAE42174	Aae42174 p53 N-ter
16	99	94.3	64	AAW07866	Aaw07866 Human p53
17	99	94.3	64	AAW48243	Aaw48243 Human p53
18	99	94.3	64	AAW57240	Aaw57240 Human p53
19	99	94.3	64	AAW42878	Aaw42878 N-termina
20	99	94.3	64	AAW42970	Aaw42970 N-termina
21	99	94.3	64	AAW94303	Aaw94303 Human MDM
22	99	94.3	68	ADB71206	Adb71206 Human p53
23	99	94.3	71	AAW47079	Aaw47079 Human p53

24	99	94.3	73	10	AEI18141	Aee18141 Human p53
25	99	94.3	73	10	AEI18142	Aee18142 Human p53
26	99	94.3	73	10	AEI18143	Aee18143 Human p53
27	99	94.3	73	10	AEI18138	Aee18138 Human p53
28	99	94.3	73	10	AEI18125	Aee18125 Human p53
29	99	94.3	73	10	AEI18137	Aee18137 Human p53
30	99	94.3	73	10	AEI18144	Aee18144 Human p53
31	99	94.3	73	10	AEI18139	Aee18139 Human p53
32	99	94.3	73	10	AEI18140	Aee18140 Human p53
33	99	94.3	161	4	AAE36683	Aab36683 Mammalian
34	99	94.3	164	4	AAE36689	Aab36689 Mammalian
35	99	94.3	211	4	AAE36685	Aab36685 Mammalian
36	99	94.3	225	4	AAE36690	Aab36690 Mammalian
37	99	94.3	241	2	AAE51872	Aae51872 Human p53
38	99	94.3	260	4	ABG03222	Abg03222 Novel hum
39	99	94.3	261	3	AAE70714	Aae70714 Human p35
40	99	94.3	283	4	ABG01512	Abg01512 Novel hum
41	99	94.3	293	7	AAE39686	Aae39686 Human p53
42	99	94.3	337	2	AAW13962	Aaw13962 Chimeric
43	99	94.3	341	8	ADN34522	Adn34522 Human p53
44	99	94.3	343	7	AAE39685	Aae39685 Human p53
45	99	94.3	353	6	AAE35350	Aae35350 Human col

## ALIGNMENTS

RESULT 1  
ID AAW82321 standard; peptide; 19 AA.  
AC AAW82321;  
AC AAW82321;  
DT 22-FEB-1999 (first entry)  
XX  
XX  
DE p53 homologue T1P peptide.  
XX  
XX p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.  
OS Synthetic.  
XX  
XX W09847919-A1.  
PD 29-OCT-1998.  
XX  
XX 20-APR-1998; 98WC-GB001140.  
PF  
PR 22-APR-1997; 97GB-00008089.  
XX  
XX (UYDU-) UNIV DUNDEE.  
PA  
PI Lane DP;  
XX  
XX WPI; 1998-609975/51.  
PT  
PT New substance with a mdm2 binding domain and coupling partner - useful  
PT for stabilising in cells without an efficient mdm2-mediated degradation  
PT pathway.  
XX  
XX  
PS Disclosure; Fig 1; 53pp; English.  
XX  
XX This sequence is a peptide homologue of a region of p53 which binds to  
XX mdm2. This peptide is used in the construction of a novel agent capable  
XX of disrupting the binding of p53 and mdm2 or inhibiting the production of  
XX mdm2 in a population of cells. This agent is also used in the preparation  
XX of a therapeutic for activating p53, where the population of cells do not  
XX overexpress mdm2. Inhibiting mdm2 production and/or inhibiting the  
XX binding of mdm2 to p53 allows levels of p53 to increase by reducing the  
XX clearance of p53 by mdm2, and can be used to activate p53 function. The  
XX agents for use in therapeutics for activating p53 can be used for the  
XX treatment of cancer, viral conditions or other conditions associated with  
XX non-functional p53

SQ Sequence 19 AA;  
Query Match 100.0%; Score 105; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDLWKLLPENG 19  
DB 1 PPLSQETFSDLWKLLPENG 19  
RESULT 2  
AAW82319  
ID AAW82319 standard; peptide; 19 AA.  
XX  
AC AAW82319;  
XX  
DT 22-FEB-1999 (first entry)  
XX  
DE p53 homologue TIP peptide.  
XX  
KM p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medication.  
XX  
OS Synthetic.  
XX  
PN WO9847525-A1.  
XX  
PD 29-OCT-1998.  
XX  
PF 20-APR-1998; 98WO-GB001144.  
XX  
PR 22-APR-1997; 97GB-00008092.  
XX  
PA (UYDU-) UNIV DUNDEE.  
XX  
PI Lane DP;  
XX  
DR WPI; 1998-609932/51.  
XX  
PT New agents which inhibit interaction of p53 and mdm2 - useful for  
PT activating p53, e.g. for treating cancers; viral conditions or other  
PT conditions associated with non functional p53 or mdm2.  
XX  
PS Disclosure; Fig 1; 52pp; English.  
XX  
XS This sequence is a peptide homologue of a region of p53 which binds to  
CC mdm2. This peptide is used in the construction of a novel agent capable  
CC of disrupting the binding of p53 and mdm2 or inhibiting the production of  
CC mdm2 in a population of cells. This agent is also used in the preparation  
CC of a therapeutic for activating p53, where the population of cells do not  
CC overexpress mdm2. Inhibiting mdm2 production and/or inhibiting the  
CC binding of mdm2 to p53 allows levels of p53 to increase by reducing the  
CC clearance of p53 by mdm2, and can be used to activate p53 function. The  
CC agents for use in therapeutics for activating p53 can be used for the  
CC treatment of cancer; viral conditions or other conditions associated with  
CC non-functional p53  
XX  
SQ Sequence 19 AA;  
Query Match 100.0%; Score 105; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDLWKLLPENG 19  
DB 1 PPLSQETFSDLWKLLPENG 19  
RESULT 3  
AAW37228  
ID AAW37228 standard; peptide; 18 AA.  
XX  
AC AAW37228;

XX  
DT 20-JUL-1998 (first entry)  
XX  
DE p53 N-terminal peptide fragment for Elisa TIP assay.  
XX  
KM MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
XX tumour; diagnosis; binding; viral infection; Elisa TIP assay.  
XX  
OS Homo sapiens.  
XX  
PN WO9801467-A2.  
XX  
PD 15-JAN-1998.  
XX  
PF 04-JUL-1997; 97WO-EP003549.  
XX  
PR 05-JUL-1996; 96GB-00014197.  
XX 07-APR-1997; 97GB-00007041.  
XX  
PA (NOVS ) NOVARTIS AG.  
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
PI Lane D, Boettger V, Boettger A, Pickslay S, Hochkeppel H;  
PI Garcia-Echeverria C, Chene P, Furet P;  
XX  
DR WPI; 1998-100996/09.  
XX  
PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
PT useful in, e.g. diagnosis and treatment of cancer and viral infections  
PT and identifying binding agents.  
XX  
PS Disclosure; Page 34; 45pp; English.  
XX  
XS This represents a p53 N-terminal peptide fragment used in an Elisa TIP  
CC assay for analysing the interaction between human oncogenic protein MDM2  
CC and p53. The invention provides peptide derivatives capable of binding to  
CC the human MDM2. These peptides can specifically inhibit or block the  
CC binding of MDM2 to the human p53 protein, in vitro or in vivo. Inhibiting  
CC the interaction between the p53 and MDM2 can induce growth arrest or  
CC apoptosis in tumour cells comprising a wild-type p53 and non-elevated  
CC levels of MDM2. The peptides may be used to identify molecules that bind  
CC to MDM2 and to identify and design inhibitors of MDM2/p53 binding. They  
CC may also be used to purify binding partners especially MDM2, diagnose  
CC disease by measuring levels of MDM2 in blood of cancer and leukaemia  
CC patients and for treatment or prevention of disease involving p53/MDM2  
CC interactions, especially tumours and viral infections. The peptides can  
CC be administered nasally, rectally, orally or by injection. By interfering  
CC with MDM2/p53 interaction, the peptides can activate p53 function and  
CC accumulation in normal cells. The peptides which mimic the MDM2 binding  
CC site in p53, have a significantly greater blocking activity compared with  
CC wild-type p53  
XX  
SQ Sequence 18 AA;  
Query Match 94.3%; Score 99; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDLWKLLPEN 18  
DB 1 PPLSQETFSDLWKLLPEN 18  
RESULT 4  
AAE30863  
ID AAE30863 standard; peptide; 20 AA.  
XX  
AC AAE30863;  
XX  
DT 24-FEB-2003 (first entry)  
XX  
DE EGFP-BOX-1 domain phospho-peptide used in the invention.  
XX

KM p53 polypeptide; p300 polypeptide; cell cycle; cell death; gene therapy;  
KM cancer; ischaemia; cytosolic; vasotropic.  
XX Unidentified.  
XX OS  
XX PN WO200265134-A2.  
XX PD 22-AUG-2002.  
XX PF 13-FEB-2002; 2002WO-GB000640.  
XX PR 13-FEB-2001; 2001GB-00003508.  
XX PA (UYDU-) UNIT DUNDEE.  
XX PI Hupp TR, Dornan D;  
XX DR WPI; 2003-018623/01.  
XX PT New peptide for modulating the binding of p53 polypeptide to p300  
XX PT polypeptide, useful for regulating the mammalian cell cycle for the  
XX PT treatment of cancer or ischemia.  
XX PS Example 1; Page 22; 87pp; English.  
XX CC The invention relates to a peptide for use in modulating the binding of a  
XX CC p53 polypeptide to a p300 polypeptide. The new peptide is useful in  
XX CC modulating the binding of a p53 polypeptide to a p300 polypeptide. The  
XX CC peptide may be used to regulate the mammalian cell cycle or to induce or  
XX CC prevent cell death, for the treatment of cancer or ischemia. The  
XX CC invention is useful in gene therapy. The present sequence is EGFP-BOX-1  
XX CC domain phospho-peptide used in the exemplification of the invention  
SQ Sequence 20 AA;  
Query Match 94.3%; Score 99; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDLWKLTPEN 18  
Db 2 PPLSQETFSDLWKLTPEN 19  
RESULT 5  
AARS4907  
ID AARS4907 standard; peptide; 25 AA.  
XX AARS4907;  
XX AC  
XX XX  
DT 25-MAR-2003 (revised)  
DT 29-NOV-1994 (first entry)  
XX  
DE Immunodominant epitope from p53 N-terminal.  
XX  
XX cancer; pre-cancerous state; detection; diagnosis; human p53 gene;  
KM immunodominant epitope; human cellular tumour antigen;  
KM transformation-associated protein.  
XX  
XX Homo sapiens.  
XX OS  
XX PN WO9410306-A1.  
XX PD 11-MAY-1994.  
XX PF 02-NOV-1993; 93WO-FR001082.  
XX PR 02-NOV-1992; 92FR-00013110.  
XX (EURO-) LAB EUROBIOT.  
XX PA  
XX PI Soussel T, Lubin R, Legros Y;  
XX

DR WPI; 1994-167463/20.  
XX  
XX New immuno:dominant epitope(s) of protein p53 - for detecting and  
PT monitoring antibodies indicative of cancer and precancerous states.  
XX  
XX PS Claim 4; Page 42; 62pp; French.  
XX  
XX Peptides derived from the N-terminal (amino acids 1-112) or the C-  
CC terminal (amino acids 350-393) of protein p53 which specifically react  
CC with anti-p53 antibodies in patients with cancer or precancerous  
CC conditions are claimed. The peptides (AARS4907-R54921) are useful for  
CC detecting and monitoring cancerous and precancerous conditions. (updated  
CC on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 25 AA;  
Query Match 94.3%; Score 99; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDLWKLTPEN 18  
Db 2 PPLSQETFSDLWKLTPEN 19  
RESULT 6  
AARS1879  
ID AARS1879 standard; protein; 25 AA.  
XX  
XX AARS1879;  
XX AC  
XX XX  
DT 25-MAR-2003 (revised)  
DT 18-NOV-1994 (first entry)  
XX  
DE Human p53 amino acids 9-33.  
XX  
XX Human nuclear phosphoprotein p53; tumour suppressor gene product;  
KM anti-oncogene; cancer; tumour; antibody binding region; epitope.  
XX  
XX Homo sapiens.  
XX OS  
XX PN WO9408241-A1.  
XX PD 14-APR-1994.  
XX PF 30-SEP-1993; 93WO-EP002666.  
XX PR 30-SEP-1992; 92DE-04232823.  
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG.  
XX PA Zentgraf H, Schranz P, Volkmann M, Tesamer C, Klein R;  
XX PI  
XX DR WPI; 1994-135732/16.  
XX DR N-PSDB; AA062365.  
XX PT Non-radioactive detection of p53 specific antibodies - by capture on  
PT immobilised p53 or its fragments, then reaction with labelled second  
XX antibody, for diagnosis of tumours and suitable for screening.  
XX  
XX Claim 11; Page 19; 35pp; German.  
XX  
XX Antibodies specific for p53 are detected by binding to immobilised  
CC fragments of the p53 gene product containing the antibody-binding region.  
CC Preferred fragments contain amino acids 1-241, 40-393, 66-241, 66  
CC -393, 237-349, 237-393 and esp. 9-33, 37-52 or 368-386. See AARS1872-  
CC R51881 for sequences of these fragments. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX  
SQ Sequence 25 AA;  
Query Match 94.3%; Score 99; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.1e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLPEN 18  
 |||||  
 DB 4 PPLSQETFSDLWKLPEN 21

## RESULT 7

AAW60202  
 ID AAW60202 standard; peptide; 26 AA.

AC AAW60202;  
 XX

DT 18-AUG-1998 (first entry)

DE p53 peptide used to detect antibodies against p53.

KW Human; p53; antibody; detection; biosensor; cancer patient;

XX p53 gene therapy; immune response; mutant.

OS Synthetic.

OS Homo sapiens.

PN WO9815834-A1.

PD 16-APR-1998.

PF 01-OCT-1997; 97WO-US016132.

PR 07-OCT-1996; 96US-0028533P.

PA (SCHE) SCHERING CORP.

P1 Mytych DT, Swanson SJ;

DR WPI; 1998-240965/21.

PT Detecting antibodies that bind p53 by reaction with immobilised p53

PT peptide(s) - attached directly to flow cells in the sensor chip of bio-

PT sensor, used to analyse serum from cancer patients, e.g. those being

PT given p53 gene therapy.

PS Claim 4; Page 5; 41pp; English.

CC Peptides AAW60202-05 are derived from human p53 protein. The present

CC peptide corresponds to residues 11-35. The peptides are used in the

CC method of the invention. Antibodies that bind to p53 protein are detected

CC by immobilising a p53 peptide directly on to a flow cell of a sensor chip

CC in a biosensor, treating the peptide with a sample of patient serum,

CC diluted in buffer, and measuring binding of antibody to the peptide using

CC the biosensor. The method is used to monitor cancer patients undergoing

CC p53 gene therapy (to determine if an immune response has developed), and

CC also to detect antibodies against mutant forms of p53

XX SQ Sequence 26 AA;

Query Match 94.3%; Score 99; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 2.2e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLPEN 18  
 |||||  
 DB 3 PPLSQETFSDLWKLPEN 20

RESULT 8  
 AAB30523  
 ID AAB30523 standard; peptide; 32 AA.  
 XX  
 AC AAB30523;  
 XX  
 DT 06-MAR-2001 (first entry)  
 XX

DE Peptide fragment of a tumour suppressor protein p53.

KW Biologically active compound; cellular metabolism; DNA replication;

KW RNA transcription; RNA translation; RNA elongation; RNA processing;

KW protein synthesis; protein processing; cellular differentiation;

KW cell division; ion channel transmission; cellular protein; toxin;

KW RNA transportation; cellular oxidation; tumour suppressor p53;

KW plasmidogen antigen activator.

OS Synthetic.

PN WO200061775-A1.

PD 19-OCT-2000.

PF 08-APR-1999; 99WO-IB000616.

PR 08-APR-1999; 99WO-IB000616.

PA (SERG/) SERGEEV P.

P1 Sergeev P;

DR WPI; 2001-006911/01.

PT Novel methods for the synthesis of biologically active compounds from

PT inactive precursors in the cells of living organisms, useful for

PT producing proteins or polynucleotides.

PS Example 8; Page 29; 65pp; English.

CC The specification describes a method of synthesis of biologically active

CC substances of determined structure directly in the cells of living

CC organisms containing specific RNA or DNA sequence. The method is based on

CC the hybridisation of two or more oligomers bound with biologically

CC inactive substances to specific RNA or DNA in vivo in the cells of living

CC organisms. After hybridisation of the oligomers, the biologically

CC inactive precursors bound to the oligomers can interact with each other

CC to make the active form of the substances. This changing of properties is

CC due to chemical reactions which bind the biologically inactive precursors

CC through a chemical bond into a biologically active form of the whole

CC compound. The methods are useful for producing biologically active

CC compounds from inactive precursors. These compounds may be inhibitors or

CC stimulators of cellular metabolism, DNA replication, RNA transcription,

CC RNA translation, RNA elongation, RNA processing, protein synthesis,

CC protein processing, cellular differentiation, cell division, ion channel

CC transmission, cellular protein and RNA transportation, processes of

CC cellular oxidation, toxins, proteins or RNAs. AAB30523-36 represent

CC peptides which are bound to oligomers AAC62167-80 and AAC62181-94. The

CC peptides are fragments of the tumour suppressor p53, and the oligomers

CC are antiparallel to human plasmidogen antigen activator mRNA (AAC62167-80) or human NBH0R (AAC62181-94). The method of the invention is used to

CC produce the tumour suppressor protein p53 from the bound peptides and

XX oligomers

XX SQ Sequence 32 AA;

Query Match 94.3%; Score 99; DB 4; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.8e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLPEN 18  
 |||||  
 DB 12 PPLSQETFSDLWKLPEN 29

RESULT 9  
 ADJ25788  
 ID ADJ25788 standard; peptide; 32 AA.  
 XX  
 AC ADJ25788;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX

```
XX MDM2 binding peptide #6.
DE ligand identification; peptide library;
KW complementary combinatorial library; MDM2.
XX
OS Synthetic.
XX US6617114-B1.
XX
XX 09-SEP-2003.
XX
XX 30-APR-1998; 98US-00069827.
XX
XX 31-OCT-1996; 96US-00740671.
XX 31-OCT-1997; 97WO-US019638.
XX 31-MAR-1998; 98US-00050359.
XX
XX (KARO-) KARO BIO AB.
XX
XX Fowlkes DM, Kay BK, Frelinger JA, Hyde-Deruysscher RP,
XX
XX WPI; 2004-068186/07.
XX
XX Identification of ligand that can mediate biological activity of target
XX protein; comprises screening first combinatorial library having first
XX member ligands for binding to target protein to identify target-binding
XX ligand(s).
XX
XX Example 3; SEQ ID NO 48; 98pp; English.
XX
XX The invention relates to a method of identifying a ligand that can
XX mediate the biological activity of target protein via inhibition of the
XX binding of target protein to a binding partner ligand comprising
XX screening first combinatorial library having first member ligands for
XX binding to target protein to identify target-binding ligand(s). The
XX method is useful for identifying ligands that can mediate the biological
XX activity of target proteins via inhibition of the binding of target
XX protein to a binding partner ligand. The invention does not require that
XX the natural binding partner be used as reagent. The need for the natural
XX binding partner is obviated with the use of complementary combinatorial
XX libraries. The present sequence is used in the exemplification of the
XX present invention.
XX
XX Sequence 32 AA;
XX
XX Query Match 94.3%; Score 99; DB 8; Length 32;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-08;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 PLSQETFSDDLWKLLPEN 18
XX |||||
XX DB 12 PLSQETFSDDLWKLLPEN 29
XX
XX RESULT 10
XX AD248535
XX AD248535 standard; peptide; 32 AA.
XX
XX AC AD248535;
XX
XX DT 16-JUN-2005 (first entry)
XX
XX DE Human p53 peptide SEQ ID NO:48.
XX
XX KW combinatorial library; peptide library; p53.
XX
XX OS Homo sapiens.
XX
XX XX US2005069951-A1.
XX
XX PD 31-MAR-2005.
XX
```

```
PF 08-SEP-2003; 2003US-00656250.
XX
XX 31-OCT-1996; 96US-00740671.
XX 31-OCT-1997; 97WO-US019638.
XX 31-MAR-1998; 98US-00050359.
XX 30-APR-1998; 98US-00069827.
XX
XX (FOWL/) FOWLKES D M.
XX (KAYB/) KAY B K.
XX (FREL/) FRELINGER J A.
XX (HYDE/) HYDE-DERUYSSCHER R P.
XX
XX Fowlkes DM, Kay BK, Frelinger JA, Hyde-Deruysscher RP,
XX
XX WPI; 2005-353255/36.
XX
XX Identifying ligand mediating activity of target protein, by screening
XX ligand libraries to obtain target-binding ligands and ligands inhibiting
XX binding of target-binding ligand to target, determining ligands
XX inhibiting activity of target.
XX
XX Example 3; SEQ ID NO 48; 108pp; English.
XX
XX The invention relates to a method (M1) for identifying a ligand which can
XX mediate the biological activity of a target protein via inhibition of the
XX binding of a target protein to a binding partner. The method comprises
XX identifying target-binding ligands by screening first member ligands of a
XX first library, obtaining ligands which inhibit the binding of target-
XX binding ligands to a target protein by screening second member ligands of
XX a second library, and determining inhibitory ligands mediating activity
XX of the target protein. Also described is a method for identifying a pair
XX of ligands, the first ligand of the pair inhibiting the binding of a target
XX to the second ligand of the pair inhibiting the binding of the first ligand
XX to the target protein, which involves: (a) screening the first
XX combinatorial library comprising several first member ligands for binding
XX to the target protein, thus identifying one or more target binding
XX ligands; and (b) screening the second library comprising several second
XX member ligands for the ability to inhibit the binding of one or more of
XX the target-binding ligands to the target protein, thus obtaining one or
XX more inhibitory ligands, where the second library is not identical to the
XX first library, the first ligand of the pair is one of the target binding
XX first member ligands of the first library, the second ligand of the pair
XX is one of the second member ligands of the second library, and when the
XX ligands are peptides, they are not more than 41 amino acids long, or they
XX do not comprise antibody-like domains. (M1) is useful for identifying a
XX ligand which can mediate the biological activity of a target protein
XX through inhibition of the binding of a target protein to a binding
XX partner. The target protein can be one associated with human
XX cytomegalovirus, DNA polymerase accessory protein UL44, human MDM2, or an
XX enzyme such as protein kinase (preferably human protein kinase C beta
XX II), a transferase, isomerase, synthetase or transfer RNA synthetase,
XX preferably PKR, where the ligand identified by (M1), is useful for
XX treating viral infection such as human cytomegalovirus infection, and
XX diseases related to aberrant expression of the above target proteins.
XX (M1) enables identification of drugs using complementary combinatorial
XX libraries, and identification of compounds in a compound library which
XX can mediate the biological activity of a target protein, even when the
XX CC ligands which mediate the activity through binding to the receptor are
XX not already known. The present sequence represents a human p53 peptide
XX which is used in an example from the present invention.
XX
XX Sequence 32 AA;
XX
XX Query Match 94.3%; Score 99; DB 9; Length 32;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-08;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 PLSQETFSDDLWKLLPEN 18
XX |||||
XX DB 12 PLSQETFSDDLWKLLPEN 29
XX
XX RESULT 11
```

```
AAW13604
ID AAW13604 standard; peptide; 36 AA.
XX
XX AAW13604;
AC
XX
XX 16-JAN-1998 (first entry)
DT
XX
XX p53 protein amino acids 6-41.
DE
XX
XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
KW restenosis.
XX
XX Homo sapiens.
OS
XX
XX WO9709343-A2.
PN
XX
XX 13-MAR-1997.
PD
XX
XX 02-SEP-1996; 96WO-FR001340.
PF
XX
XX 04-SEP-1995; 95FR-00010331.
PR
XX
XX (RHON ) RHONE POULENC RORER SA.
PA (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
XX
XX Tocque B, Dubs-Poterszman M, Wasyluk B;
PI
XX
XX WPI; 1997-192837/17.
DR
XX
XX Treating cancer with antagonist of oncogenic activity of protein Mdm2 -
PT or nucleic acid encoding an antagonist, also viral vectors contg. this
XX nucleic acid.
XX
XX Claim 4; Page; 43pp; French.
XX
XX The peptides AAW13602-6 represent peptide fragments derived from the wild
CC type human p53 protein. This peptide corresponds to amino acids 6-41 of
CC the p53 sequence. The peptides are claimed peptides which are able to
CC bind the N-terminal amino acids (1-134) of the murine double minute-2
CC (mdm2) protein (AAW13600). Mdm2 protein is a 90 kD phosphoprotein which
CC binds and modulates the activity of the tumour suppressor protein p53. It
CC has now been shown that the mdm2 protein itself has oncogenic properties,
CC especially in a p53-null background. Mdm2 is observed to unblock cell
CC cycle arrest in G1 caused by over-expression of the p107 protein. The p53
CC peptides are examples of antagonists of the invention which are able to
CC inhibit the oncogenic activity of mdm2. The antagonists are used to treat
CC e.g. adenocarcinoma of the colon; cancer of the breast; lung or stomach;
CC myeloid leukaemia; B cell lymphoma; or other hyperproliferative
CC conditions such as restenosis. Note: this sequence is not given in the
CC specification but is constructed from the wild type human p53 sequence
XX
XX
XX Sequence 36 AA;
SQ
Query Match 94.3%; Score 99; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PPLSQETFSDLWKLLPEN 18
DB 7 PPLSQETFSDLWKLLPEN 24
RESULT 12
AAW13603
ID AAW13603 standard; peptide; 41 AA.
XX
XX AAW13603;
AC
XX
XX 16-JAN-1998 (first entry)
DT
XX
```

```
DE p53 protein amino acids 1-41.
XX
XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
KW restenosis.
XX
XX Homo sapiens.
OS
XX
XX WO9709343-A2.
PN
XX
XX 13-MAR-1997.
PD
XX
XX 02-SEP-1996; 96WO-FR001340.
PF
XX
XX 04-SEP-1995; 95FR-00010331.
PR
XX
XX (RHON ) RHONE POULENC RORER SA.
PA (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
XX
XX Tocque B, Dubs-Poterszman M, Wasyluk B;
PI
XX
XX WPI; 1997-192837/17.
DR
XX
XX Treating cancer with antagonist of oncogenic activity of protein Mdm2 -
PT or nucleic acid encoding an antagonist, also viral vectors contg. this
XX nucleic acid.
XX
XX Claim 4; Page; 43pp; French.
XX
XX The peptides AAW13602-6 represent peptide fragments derived from the wild
CC type human p53 protein. This peptide corresponds to amino acids 1-41 of
CC the p53 sequence. The peptides are claimed peptides which are able to
CC bind the N-terminal amino acids (1-134) of the murine double minute-2
CC (mdm2) protein (AAW13600). Mdm2 protein is a 90 kD phosphoprotein which
CC binds and modulates the activity of the tumour suppressor protein p53. It
CC has now been shown that the mdm2 protein itself has oncogenic properties,
CC especially in a p53-null background. Mdm2 is observed to unblock cell
CC cycle arrest in G1 caused by over-expression of the p107 protein. The p53
CC peptides are examples of antagonists of the invention which are able to
CC inhibit the oncogenic activity of mdm2. The antagonists are used to treat
CC e.g. adenocarcinoma of the colon; cancer of the breast; lung or stomach;
CC myeloid leukaemia; B cell lymphoma; or other hyperproliferative
CC conditions such as restenosis. Note: this sequence is not given in the
CC specification but is constructed from the wild type human p53 sequence
XX
XX
XX Sequence 41 AA;
SQ
Query Match 94.3%; Score 99; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PPLSQETFSDLWKLLPEN 18
DB 12 PPLSQETFSDLWKLLPEN 29
RESULT 13
ADT02859
ID ADT02859 standard; protein; 50 AA.
XX
XX ADT02859;
AC
XX
XX 02-DEC-2004 (first entry)
DT
XX
XX Human p53 protein fragment, target of an immunoassay SeqID 1.
DE
XX
XX immunoassay; autoantibody; p53; human.
KW
XX
XX Homo sapiens.
OS
XX
XX JP2004231535-A.
PN
```

XX 19-AUG-2004.  
PD  
XX 29-JAN-2003; 2003JP-00019760.  
PF  
XX 29-JAN-2003; 2003JP-00019760.  
PR  
XX (SANN ) SANYO CHEM IND LTD.  
XX  
XX WPI; 2004-618712/60.  
DR  
XX  
XX  
PT Reagent for performing immunoassay for detecting autoantibody against p53  
PT gene product, comprises amino acid sequence, in which 8-50 amino acids  
PT are essential structural unit.  
XX  
XX  
PS Claim 1; SEQ ID NO 1; 91pp; Japanese.  
XX  
CC This invention relates to a novel reagent used for performing an  
CC immunoassay for detecting autoantibodies with respect to the p53 gene  
CC product. Specifically, it refers to a sandwich method that involves  
CC assaying an anti-human immunoglobulin antibody to determine the presence  
CC or absence of an autoantibody with respect to the p53 gene product in a  
CC test substance (such as blood) and comparing these values with a standard  
CC control from a healthy subject. The present invention describes a method  
CC based on a chemiluminescent enzyme immunoassay. As such, it provides an  
CC accurate and sensitive assay that can be used to detect and diagnose a  
CC cancer state. This polypeptide sequence is a human p53 protein fragment.  
CC  
XX  
SQ Sequence 50 AA;  
Query Match 94.3%; Score 99; DB 8; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 PPLSOETFSDLWKLPEN 18  
7 PPLSOETFSDLWKLPEN 24  
XX  
RESULT 14  
AAW13602  
ID AAW13602 standard; peptide; 52 AA.  
XX  
AC AAW13602;  
XX  
DT 16-JAN-1998 (first entry)  
XX  
XX p53 protein amino acids 1-52.  
DE  
XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;  
XX tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;  
XX inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;  
XX lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;  
XX restenosis.  
XX  
XX Homo sapiens.  
XX  
XX WO9709343-A2.  
XX  
PD 13-MAR-1997.  
XX  
XX 02-SEP-1996; 96WO-FR001340.  
XX  
XX 04-SEP-1995; 95FR-00010331.  
XX  
XX (RHON ) RHONE-POULENC ROBER SA.  
XX (INRM ) INST NAT SANTE & RECH MEDICALE.  
XX  
XX Tocque B. Dubs-Poterezman M. Wasylyk B;  
XX  
XX WPI; 1997-192837/17.  
XX

PT Treating cancer with antagonist of oncogenic activity of protein Mdm2 -  
PT or nucleic acid encoding an antagonist, also viral vectors contg. this  
PT nucleic acid.  
XX  
XX Claim 4; Page; 43pp; French.  
PS  
XX The peptides AAW13602-6 represent peptide fragments derived from the wild  
CC type human p53 protein. This peptide corresponds to amino acids 1-52 of  
CC the p53 sequence. The peptides are claimed peptides which are able to  
CC bind the N-terminal amino acids (1-134) of the murine double minute-2  
CC (mdm2) protein (AAW13600). Mdm2 protein is a 90 kD phosphoprotein which  
CC binds and modulates the activity of the tumour suppressor protein p53. It  
CC has now been shown that the mdm2 protein itself has oncogenic properties,  
CC especially in a p53-null background. Mdm2 is observed to unblock cell  
CC cycle arrest in G1 caused by over-expression of the p107 protein. The p53  
CC peptides are examples of antagonists of the invention which are able to  
CC inhibit the oncogenic activity of mdm2. The antagonists are used to treat  
CC e.g. adenocarcinoma of the colon; cancer of the breast; lung or stomach;  
CC myeloid leukaemia; B cell lymphoma; or other hyperproliferative  
CC conditions such as restenosis. Note: this sequence is not given in the  
CC specification but is constructed from the wild type human p53 sequence  
XX  
SQ Sequence 52 AA;  
Query Match 94.3%; Score 99; DB 2; Length 52;  
Best Local Similarity 100.0%; Pred. No. 4.7e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 PPLSOETFSDLWKLPEN 18  
12 PPLSOETFSDLWKLPEN 29  
XX  
RESULT 15  
AAR42174  
ID AAR42174 standard; peptide; 64 AA.  
XX  
AC AAR42174;  
XX  
DT 25-MAR-2003 (revised)  
DT 05-MAY-1994 (first entry)  
XX  
XX p53 N-terminal fragment.  
DE  
XX p53 gene; tumour suppressor gene; regulation; cellular proliferation;  
XX cellular transformation; carcinoma; human; tumour; MDM2; inhibition;  
XX gene amplification.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Binding-site 13..41  
XX /note="Site of interaction with MDW-2"  
XX  
XX WO9320238-A2.  
XX  
XX 14-OCT-1993.  
XX  
XX 07-APR-1993; 93WO-US003199.  
XX  
XX 07-APR-1992; 92US-00867840.  
XX 23-JUN-1992; 92US-00903103.  
XX  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX Burrell M, Hill DE, Kinzler KM, Vogelstein B;  
XX  
XX WPI; 1993-336944/42.  
XX  
XX Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene  
XX expression, also new DNA, MDM2 protein, antibodies and treatment of  
XX sarcoma by inhibiting MDM2 expression.  
XX

PS Disclosure; Page 35; 75pp; English.  
XX  
CC This sequence represents the product of the p53 gene. p53 is a tumour  
CC suppressor gene and this protein appears to be a member of a group of  
CC proteins which regulate normal cellular proliferation and suppression of  
CC cellular transformation. Inactivation of the p53 gene has been implicated  
CC in the formation, or progression of a wide variety of carcinoma. p53 is  
CC thought to interact with the protein product of a gene which is amplified  
CC in a number of human tumours, designated MDM2. Polypeptides containing at  
CC least amino acids 13-41 of p53, or the DNA encoding these, may be used to  
CC inhibit the growth of tumour cells containing MDM2 gene amplification.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 64 AA;

Query Match 94.3%; Score 99; DB 2; Length 64;  
Best Local Similarity 100.0%; Pred. No. 5,9e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDDLWKLLPEN 18  
|||||  
DB 12 PPLSQETFSDDLWKLLPEN 29

Search completed: July 5, 2006, 22:40:46  
Job time : 198 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 5, 2006, 22:46:46 ; Search time 184 Seconds  
(without alignments)  
47.832 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105  
Sequence: 1 PPLSQETFSDDLWKLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:  
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2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	99	94.3	18	3	US-09-214-371-74
2	99	94.3	18	5	US-10-927-262A-74
3	99	94.3	20	4	US-10-155-059-8
4	99	94.3	20	4	US-10-155-059-10
5	99	94.3	20	4	US-10-155-059-11
6	99	94.3	20	4	US-10-155-059-16
7	99	94.3	20	4	US-10-467-758-8
8	99	94.3	32	3	US-09-958-163A-3
9	99	94.3	32	5	US-10-918-643-3
10	99	94.3	32	5	US-10-656-250-48
11	99	94.3	260	5	US-10-450-763-33581
12	99	94.3	283	5	US-10-450-763-31871
13	99	94.3	327	6	US-10-450-763-014-24
14	99	94.3	353	3	US-09-849-602-24
15	99	94.3	353	4	US-10-146-473-78
16	99	94.3	358	4	US-10-696-255A-8
17	99	94.3	386	4	US-10-444-287-2
18	99	94.3	386	4	US-10-696-255A-7
19	99	94.3	392	4	US-10-696-255A-2
20	99	94.3	393	3	US-09-776-695-32
21	99	94.3	393	3	US-09-732-384-3
22	99	94.3	393	3	US-09-860-211-9
23	99	94.3	393	3	US-09-829-327-4
24	99	94.3	393	3	US-09-860-286-9
25	99	94.3	393	3	US-09-829-922-2
26	99	94.3	393	3	US-09-860-286-9
27	99	94.3	393	4	US-10-274-874-4

28	99	94.3	393	4	US-10-160-290-2	Sequence 2, Appl1
29	99	94.3	393	4	US-10-077-176-54	Sequence 54, Appl1
30	99	94.3	393	4	US-10-077-176-55	Sequence 55, Appl1
31	99	94.3	393	4	US-10-077-176-56	Sequence 56, Appl1
32	99	94.3	393	4	US-10-077-176-57	Sequence 57, Appl1
33	99	94.3	393	4	US-10-434-693-2	Sequence 2, Appl1
34	99	94.3	393	4	US-10-392-113-31	Sequence 31, Appl1
35	99	94.3	393	4	US-10-165-216-4	Sequence 4, Appl1
36	99	94.3	393	4	US-10-191-121-3	Sequence 3, Appl1
37	99	94.3	393	4	US-10-339-712-49	Sequence 49, Appl1
38	99	94.3	393	4	US-10-391-068-2	Sequence 2, Appl1
39	99	94.3	393	4	US-10-441-510-9	Sequence 9, Appl1
40	99	94.3	393	4	US-10-633-789-1	Sequence 1, Appl1
41	99	94.3	393	4	US-10-716-359-25	Sequence 25, Appl1
42	99	94.3	393	4	US-10-340-179-20	Sequence 20, Appl1
43	99	94.3	393	4	US-10-773-714-33	Sequence 33, Appl1
44	99	94.3	393	4	US-10-724-225-4	Sequence 4, Appl1
45	99	94.3	393	5	US-10-456-238-4	Sequence 4, Appl1

#### ALIGNMENTS

```
RESULT 1
US-09-214-371-74
; Sequence 74, Application US/09214371B
; Patent No. US2001001851A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Botteger, Volker
; APPLICANT: Botteger, Angelica
; APPLICANT: Picklesley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Scheverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-74

Query Match          94.3% Score 99; DB 3; Length 18;
Best Local Similarity 100.0% Pred. No. 9.7e+08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PPLSQETFSDDLWKLPEN 18
Db      1 PPLSQETFSDDLWKLPEN 18

RESULT 2
US-10-927-262A-74
; Sequence 74, Application US/10927262A
; Publication No. US20050137137A1
; GENERAL INFORMATION:
; APPLICANT: LANE, DAVID P
; APPLICANT: BOTTEGER, VOLKER
; APPLICANT: BOTTEGER, ANGELICA
; APPLICANT: PICKLESLEY, STEVEN M.
; APPLICANT: HOCHKEPPEL, HEINZ-KURT
; APPLICANT: GARCIA-SCHEVERRIA, CARLOS
; APPLICANT: CHENE, PATRICK
```

APPLICANT: FURET, PASCAL  
TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2  
FILE REFERENCE: 39749.0002 APC CON  
CURRENT APPLICATION NUMBER: US/10/927,262A  
CURRENT FILING DATE: 2004-08-25  
PRIOR APPLICATION NUMBER: 09/214,371  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: PCT/EP97/03549  
PRIOR FILING DATE: 1997-07-04  
PRIOR APPLICATION NUMBER: GB 9614197.3  
PRIOR FILING DATE: 1996-07-05  
PRIOR APPLICATION NUMBER: GB 9707041.1  
PRIOR FILING DATE: 1997-04-07  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 74  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-927-262A-74

Query Match 94.3%; Score 99; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.7e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSOETFSDLWKLPEN 18  
1 PPLSOETFSDLWKLPEN 18

Db 1 PPLSOETFSDLWKLPEN 18

RESULT 3  
US-10-155-059-8  
Sequence 8, Application US/10155059  
Publication No. US20020147173A1  
GENERAL INFORMATION:  
APPLICANT: Kaelin, William  
Jost, Christine  
TITLE OF INVENTION: METHODS OF TREATMENT USING  
NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
ANTIBODIES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon Peabody LLP  
STREET: 101 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/155,059  
FILING DATE: 24-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,975  
FILING DATE: 12-May-1998  
APPLICATION NUMBER: 60/046,207  
FILING DATE: 12-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-10-155-059-8

Query Match 94.3%; Score 99; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSOETFSDLWKLPEN 18  
2 PPLSOETFSDLWKLPEN 19

Db 2 PPLSOETFSDLWKLPEN 19

RESULT 4  
US-10-155-059-10  
Sequence 10, Application US/10155059  
Publication No. US20020147173A1  
GENERAL INFORMATION:  
APPLICANT: Kaelin, William  
Jost, Christine  
TITLE OF INVENTION: METHODS OF TREATMENT USING  
NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
ANTIBODIES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon Peabody LLP  
STREET: 101 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/155,059  
FILING DATE: 24-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,975  
FILING DATE: 12-May-1998  
APPLICATION NUMBER: 60/046,207  
FILING DATE: 12-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-155-059-10

Query Match 94.3%; Score 99; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSOETFSDLWKLPEN 18  
1 PPLSOETFSDLWKLPEN 18

Db 2 PPLSQETFSDLWKLPEN 19

RESULT 5  
US-10-155-059-11  
; Sequence 11, Application US/10155059  
; Publication No. US20020147173A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; ; Joet, Christine  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
; ANTIBODIES

NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon Peabody LLP  
STREET: 101 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/155,059  
FILING DATE: 24-May-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,975  
FILING DATE: 12-MAY-1998  
APPLICATION NUMBER: 60/046,207  
FILING DATE: 12-MAY-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-155-059-11

Query Match 94.3%; Score 99; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1,1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPEN 18  
Db 2 PPLSQETFSDLWKLPEN 19

RESULT 6  
US-10-155-059-16  
; Sequence 16, Application US/10155059  
; Publication No. US20020147173A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; ; Joet, Christine  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
; ANTIBODIES

NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon Peabody LLP  
STREET: 101 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/155,059  
FILING DATE: 24-May-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,975  
FILING DATE: 12-MAY-1998  
APPLICATION NUMBER: 60/046,207  
FILING DATE: 12-MAY-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-10-155-059-16

Query Match 94.3%; Score 99; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1,1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPEN 18  
Db 2 PPLSQETFSDLWKLPEN 19

RESULT 7  
US-10-467-758-8  
; Sequence 8, Application US/10467758  
; Publication No. US20040132108A1  
; GENERAL INFORMATION:  
; APPLICANT: Hupp, Theodore  
; ; Dorman, David  
; TITLE OF INVENTION: Screening Method and Agents  
; FILE REFERENCE: 9013.54  
; CURRENT APPLICATION NUMBER: US/10/467,758  
; PRIOR FILING DATE: 2003-08-13  
; PRIOR APPLICATION NUMBER: PCT/GB02/00640  
; PRIOR FILING DATE: 2002-02-13  
; PRIOR APPLICATION NUMBER: GB 0103508.8  
; PRIOR FILING DATE: 2001-02-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 8  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: EGFP BOX-1 PEPTIDE  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: RESIDUE MAY OPTIONALLY BE PHOSPHORYLATED



TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 790CIP3/US  
CURRENT APPLICATION NUMBER: US/10/450,763  
CURRENT FILING DATE: 2003-06-11  
PRIOR APPLICATION NUMBER: PCT/US01/08631  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 60736  
SOFTWARE: Custom  
SEQ ID NO 33581  
LENGTH: 260  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (97)..(137)  
OTHER INFORMATION: p53 tumor antigen proteins domain identified by eMATRIX,  
accession number BL00348B, p-value=1.000e-40, raw score of 12.18  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (7)..(255)  
OTHER INFORMATION: p53 domain identified by Pfam, accession name P53, E-value=  
US-10-450-763-33581

Query Match 94.3%; Score 99; DB 5; Length 260;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDDLWKLPEN 18  
Db 12 PPLSQETFSDDLWKLPEN 29

RESULT 12  
US-10-450-763-31871  
Sequence 31871, Application US/10450763  
Publication No. US20050196754A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 790CIP3/US  
CURRENT APPLICATION NUMBER: US/10/450,763  
CURRENT FILING DATE: 2003-06-11  
PRIOR APPLICATION NUMBER: PCT/US01/08631  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 60736  
SOFTWARE: Custom  
SEQ ID NO 31871  
LENGTH: 283  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (151)..(173)  
OTHER INFORMATION: P53 TUMOR SUPPRESSOR SIGNATURE domain identified by eMATRIX,  
accession number PR00386B, p-value=5.950e-30, raw score of 12.28  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (7)..(281)  
OTHER INFORMATION: p53 domain identified by Pfam, accession name P53, E-value=  
US-10-450-763-31871

Query Match 94.3%; Score 99; DB 5; Length 283;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDDLWKLPEN 18  
Db 12 PPLSQETFSDDLWKLPEN 29

RESULT 13  
US-11-236-014-24  
Sequence 24, Application US/11236014  
Publication No. US20060062792A1  
GENERAL INFORMATION:  
APPLICANT: Deppe, Wolfgang W.  
TITLE OF INVENTION: Novel Human p53 Splice Variant Displaying Differential  
Transcriptional Activity  
FILE REFERENCE: 4121-178  
CURRENT APPLICATION NUMBER: US/11/236,014  
CURRENT FILING DATE: 2005-09-27  
PRIOR APPLICATION NUMBER: PCT/EP2004/003299  
PRIOR FILING DATE: 2004-03-27  
PRIOR APPLICATION NUMBER: EP 0307000.7  
PRIOR FILING DATE: 2003-03-27  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 24  
LENGTH: 327  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-236-014-24

Query Match 94.3%; Score 99; DB 6; Length 327;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDDLWKLPEN 18  
Db 12 PPLSQETFSDDLWKLPEN 29

RESULT 14  
US-09-849-602-24  
Sequence 24, Application US/09849602  
Publication No. US20030165834A1  
GENERAL INFORMATION:  
APPLICANT: Scianlan, Matthew J.  
APPLICANT: Old, Lloyd J.  
APPLICANT: Stockert, Elisabeth  
APPLICANT: Chen, Yao-Tseng  
TITLE OF INVENTION: Colon Cancer Antigen Panel  
FILE REFERENCE: L0461/7105(CRV)  
CURRENT APPLICATION NUMBER: US/09/849,602  
CURRENT FILING DATE: 2001-05-04  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 24  
LENGTH: 353  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (76)..(76)  
OTHER INFORMATION: X = any amino acid  
US-09-849-602-24

Query Match 94.3%; Score 99; DB 3; Length 353;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDDLWKLPEN 18  
Db 12 PPLSQETFSDDLWKLPEN 29



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OM protein - protein search, using sw model

Run on: July 5, 2006, 22:47:41 ; Search time 20 Seconds  
(without alignments)  
25.490 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105  
Sequence: 1 PPLSQETFSDDLWKLPEN 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New\*

1: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US09\_NEW\_PUB.pep.\*  
2: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US06\_NEW\_PUB.pep.\*  
3: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US07\_NEW\_PUB.pep.\*  
4: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US08\_NEW\_PUB.pep.\*  
5: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/PCT\_NEW\_PUB.pep.\*  
6: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US10\_NEW\_PUB.pep.\*  
7: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US11\_NEW\_PUB.pep.\*  
8: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	94.3	393	6 US-10-538-066-367	Sequence 367, App
2	99	94.3	393	7 US-11-315-777-9	Sequence 9, Appl1
3	99	94.3	393	7 US-11-340-715-3	Sequence 3, Appl1
4	99	94.3	393	7 US-11-009-357-6	Sequence 6, Appl1
5	99	94.3	393	7 US-11-319-873-9	Sequence 9, Appl1
6	99	94.3	425	7 US-11-009-357-2	Sequence 2, Appl1
7	66	62.9	12	6 US-10-953-613C-778	Sequence 778, App
8	66	62.9	12	6 US-10-953-613C-790	Sequence 790, App
9	61	58.1	12	6 US-10-953-613C-780	Sequence 780, App
10	61	58.1	12	6 US-10-953-613C-792	Sequence 792, App
11	60	57.1	12	6 US-10-953-613C-779	Sequence 779, App
12	60	57.1	12	6 US-10-953-613C-791	Sequence 791, App
13	59	56.2	11	6 US-10-538-066-624	Sequence 624, App
14	55	52.4	10	6 US-10-538-066-600	Sequence 600, App
15	55	52.4	12	6 US-10-953-613C-781	Sequence 781, App
16	55	52.4	12	6 US-10-953-613C-793	Sequence 793, App
17	49	46.7	9	6 US-10-538-066-353	Sequence 353, App
18	49	46.7	600	6 US-10-449-902-50286	Sequence 50286, A
19	47	44.8	309	6 US-10-449-902-48756	Sequence 48756, A
20	47	44.8	323	1 US-09-949-825-132	Sequence 132, App
21	47	44.8	337	1 US-09-949-825-241	Sequence 241, App
22	47	44.8	6	US-10-449-902-55791	Sequence 55791, A
23	46	43.8	621	6 US-10-449-902-53028	Sequence 53028, A
24	46	43.8	812	7 US-11-293-697-3673	Sequence 3673, Ap
25	45.5	43.3	266	6 US-10-953-349-1960	Sequence 1960, Ap

26	45	42.9	338	6 US-10-953-349-5777	Sequence 5777, Ap
27	45	42.9	367	6 US-10-953-349-5776	Sequence 5776, Ap
28	45	42.9	391	6 US-10-953-349-5775	Sequence 5775, Ap
29	44	41.9	439	6 US-10-449-902-33353	Sequence 33353, A
30	44	41.9	459	6 US-10-449-902-42702	Sequence 42702, A
31	44	41.9	726	6 US-10-449-902-51533	Sequence 51533, A
32	44	41.9	726	6 US-10-449-902-56115	Sequence 56115, A
33	44	41.9	726	6 US-10-449-902-56500	Sequence 56500, A
34	43	41.0	312	6 US-10-538-066-623	Sequence 623, App
35	43	41.0	322	6 US-10-449-902-49787	Sequence 49787, App
36	42.5	40.5	603	7 US-11-293-697-2548	Sequence 2548, Ap
37	42	40.0	9	6 US-10-538-066-354	Sequence 354, App
38	42	40.0	81	6 US-10-953-349-18620	Sequence 18620, A
39	42	40.0	113	6 US-10-953-349-18617	Sequence 18617, A
40	42	40.0	191	6 US-10-953-349-20975	Sequence 20975, A
41	42	40.0	244	6 US-10-953-349-20974	Sequence 20974, A
42	42	40.0	280	6 US-10-449-902-46136	Sequence 46136, A
43	42	40.0	312	6 US-10-953-349-20973	Sequence 20973, A
44	42	40.0	538	6 US-10-953-349-35956	Sequence 35956, A
45	42	40.0	540	6 US-10-953-349-35955	Sequence 35955, A

## ALIGNMENTS

RESULT 1  
US-10-538-066-367  
Sequence 367, Application US/10538066  
Publication No. US20060094649A1  
GENERAL INFORMATION:  
APPLICANT: Epimmune Inc.  
TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen  
FILE REFERENCE: 2060.015PC06  
CURRENT APPLICATION NUMBER: US/10/538, 066  
PRIOR FILING DATE: 2005-06-09  
PRIORITY APPLICATION NUMBER: US 60/432, 017  
PRIOR FILING DATE: 2002-12-10  
NUMBER OF SEQ ID NOS: 767  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 367  
LENGTH: 393  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-538-066-367

Query Match 94.3% Score 99; DB 6; Length 393;  
Best Local Similarity 100.0%; Pred. No. 2.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDDLWKLPEN 18  
|||||  
Db 12 PPLSQETFSDDLWKLPEN 29

RESULT 2  
US-11-315-777-9  
Sequence 9, Application US/11315777  
Publication No. US20060099187A1

GENERAL INFORMATION:  
APPLICANT: Gregory, Richard J.  
Wills, Ken N.  
Maneval, Daniel C.

TITLE OF INVENTION: Recombinant Adenoviral Vector and  
Methods of Use

NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/315,777
FILING DATE: 21-Dec-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/860,286
FILING DATE: 18-May-2001
APPLICATION NUMBER: US/08/328,673
FILING DATE: 25-Oct-1994
APPLICATION NUMBER: US 08/142,669
FILING DATE: 25-Oct-1993
APPLICATION NUMBER: US 08/233,669
FILING DATE: 26-Apr-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy S.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 016930-000920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..393
OTHER INFORMATION: /note="human p53"
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-11-315-777-9

Query Match          94.3%; Score 99; DB 7; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PPLSOFPSDLWKLPEN 18
DB      12 PPLSOFPSDLWKLPEN 29

RESULT 3
US-11-340-715-3
; Sequence 3, Application US/11340715
; Publication No. US20060115852A1
; GENERAL INFORMATION:
; APPLICANT: IKAWA, Yoji
; APPLICANT: IKAWA, Shuntaro
; APPLICANT: OGINATA, Masuo
; TITLE OF INVENTION: HUMAN P51 GENES AND GENE PRODUCTS THEREOF
; FILE REFERENCE: 061014
; CURRENT APPLICATION NUMBER: US/11/340,715
; CURRENT FILING DATE: 2006-01-27
; PRIOR APPLICATION NUMBER: US/08/670,568
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: JP 10-100467
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: PCT/JP99/01512
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-340-715-3
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Query Match          94.3%; Score 99; DB 7; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PPLSOFPSDLWKLPEN 18
DB      12 PPLSOFPSDLWKLPEN 29

RESULT 4
US-11-009-357-6
; Sequence 6, Application US/11009357
; Publication No. US20060127376A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Ute
; TITLE OF INVENTION: Methods and Compositions for Modulating Apoptotic Pathways
; FILE REFERENCE: STONYB-09615
; CURRENT APPLICATION NUMBER: US/11/009,357
; CURRENT FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 6
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-357-6

Query Match          94.3%; Score 99; DB 7; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PPLSOFPSDLWKLPEN 18
DB      12 PPLSOFPSDLWKLPEN 29

RESULT 5
US-11-319-873-9
; Sequence 9, Application US/11319873
; Publication No. US20060140910A1
; GENERAL INFORMATION:
; APPLICANT: Gregory, Richard J.
; APPLICANT: Wills, Ken N.
; APPLICANT: Maneval, Daniel C.
; TITLE OF INVENTION: Recombinant Adenoviral Vector and
; Methods of Use
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/319,873
FILING DATE: 27-Dec-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/958,570
FILING DATE: 28-Oct-1997
APPLICATION NUMBER: US/08/328,673
FILING DATE: 25-Oct-1994
APPLICATION NUMBER: US 08/142,669
FILING DATE: 25-Oct-1993
APPLICATION NUMBER: US 08/233,669
FILING DATE: 26-Apr-1994
```

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;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, Timothy S.
;   REGISTRATION NUMBER: 35,367
;   REFERENCE/DOCKET NUMBER: 016930-000920US
;
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 393 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; FEATURE:
;   NAME/KEY: Protein
;   LOCATION: 1..393
;   OTHER INFORMATION: /note="human p53"
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; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-11-319-873-9

Query Match          94.3%; Score 99; DB 7; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDDLWKLLPEN 18
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DB 12 PPLSQETFSDDLWKLLPEN 29

RESULT 6
US-11-009-357-2
; Sequence 2, Application US/11009357
; Publication No. US20060127376A1
; GENERAL INFORMATION:
;   APPLICANT: Moll, Ute
;   TITLE OF INVENTION: Methods and Compositions for Modulating Apoptotic Pathways
;   FILE REFERENCE: STONYB-09615
;   CURRENT APPLICATION NUMBER: US/11/009,357
;   CURRENT FILING DATE: 2004-12-10
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: PatentIn version 3.3
;   SEQ ID NO 2
;   LENGTH: 425
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;
US-11-009-357-2

Query Match          94.3%; Score 99; DB 7; Length 425;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDDLWKLLPEN 18
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DB 12 PPLSQETFSDDLWKLLPEN 29

RESULT 7
US-10-953-613C-778
; Sequence 778, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
;   APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallion;
;   APPLICANT: Bernard;Nespor; Thomas
;   TITLE OF INVENTION: HINCE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
;   FILE REFERENCE: CEN5038 NP
;   CURRENT APPLICATION NUMBER: US/10/953,613C
;   CURRENT FILING DATE: 2004-09-29
;   PRIOR APPLICATION NUMBER: 60/507,231
;   PRIOR FILING DATE: 2003-09-30
;   NUMBER OF SEQ ID NOS: 1021
;   SOFTWARE: PatentIn Ver 3.0
;   SEQ ID NO 778
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;
US-10-953-613C-778
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;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;
US-10-953-613C-778

Query Match          62.9%; Score 66; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDDLWKLLP 16
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DB 1 QETFSDDLWKLLP 12

RESULT 8
US-10-953-613C-790
; Sequence 790, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
;   APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallion;
;   APPLICANT: Bernard;Nespor; Thomas
;   TITLE OF INVENTION: HINCE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
;   FILE REFERENCE: CEN5038 NP
;   CURRENT APPLICATION NUMBER: US/10/953,613C
;   CURRENT FILING DATE: 2004-09-29
;   PRIOR APPLICATION NUMBER: 60/507,231
;   PRIOR FILING DATE: 2003-09-30
;   NUMBER OF SEQ ID NOS: 1021
;   SOFTWARE: PatentIn Ver 3.0
;   SEQ ID NO 790
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;
US-10-953-613C-790

Query Match          62.9%; Score 66; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDDLWKLLP 16
    |||||
DB 1 QETFSDDLWKLLP 12

RESULT 9
US-10-953-613C-780
; Sequence 780, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
;   APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallion;
;   APPLICANT: Bernard;Nespor; Thomas
;   TITLE OF INVENTION: HINCE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
;   FILE REFERENCE: CEN5038 NP
;   CURRENT APPLICATION NUMBER: US/10/953,613C
;   CURRENT FILING DATE: 2004-09-29
;   PRIOR APPLICATION NUMBER: 60/507,231
;   PRIOR FILING DATE: 2003-09-30
;   NUMBER OF SEQ ID NOS: 1021
;   SOFTWARE: PatentIn Ver 3.0
;   SEQ ID NO 780
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;
US-10-953-613C-780

Query Match          58.1%; Score 61; DB 6; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.003;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 QETFSDDLWKLLP 16
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DB 1 QETFSDDLWKLLP 12
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RESULT 10
US-10-953-613C-792
; Sequence 792, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heaver, George;Knight, David;Grayeb, John;Scallon,
; APPLICANT: Bernard;Nesspor, Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CENS038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; PRIOR FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 792
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-792

Query Match      58.1%; Score 61; DB 6; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.003;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 QETFSDLWKLLP 16
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Db      1 QETFSDWKLLP 12

RESULT 11
US-10-953-613C-779
; Sequence 779, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heaver, George;Knight, David;Grayeb, John;Scallon;
; APPLICANT: Bernard;Nesspor, Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CENS038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; PRIOR FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 779
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-779

Query Match      57.1%; Score 60; DB 6; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 QETFSDLWKLLP 16
        |||||
Db      1 QETFSDLWKLLP 12

RESULT 12
US-10-953-613C-791
; Sequence 791, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heaver, George;Knight, David;Grayeb, John;Scallon;
; APPLICANT: Bernard;Nesspor, Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CENS038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; PRIOR FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231

; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 791
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-791

; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 791
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-791

Query Match      57.1%; Score 60; DB 6; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 QETFSDLWKLLP 16
        |||||
Db      1 QETFSDLWKLLP 12

RESULT 13
US-10-538-066-624
; Sequence 624, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; PRIOR FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 624
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-624

Query Match      56.2%; Score 59; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QETFSDLWKLL 15
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Db      1 QETFSDLWKLL 11

RESULT 14
US-10-538-066-600
; Sequence 600, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; PRIOR FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 600
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-600

Query Match      52.4%; Score 55; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 5 QETFSDLWKL 14  
 Db 1 QETFSDLWKL 10

RESULT 15

US-10-953-613C-781  
 ; Sequence 781, Application US/10953613C  
 ; Publication No. US20060127404A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallion;  
 ; APPLICANT: Bernard;Nespor; Thomas  
 ; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES  
 ; FILE REFERENCE: CEN5038 NP  
 ; CURRENT APPLICATION NUMBER: US/10/953,613C  
 ; CURRENT FILING DATE: 2004-09-29  
 ; PRIOR APPLICATION NUMBER: 60/507,231  
 ; PRIOR FILING DATE: 2003-09-30  
 ; NUMBER OF SEQ ID NOS: 1021  
 ; SOFTWARE: PatentIn Ver 3.0  
 ; SEQ ID NO 781  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-953-613C-781

Query Match 52.4%; Score 55; DB 6; Length 12;  
 Best Local Similarity 83.3%; Pred. No. 0.023;  
 Matches 10; Conservative 0; Mismatches 2; Indels 0;

QY 5 QETFSDLWKLIP 16  
 Db 1 QETFSDLWKLIP 12

Search completed: July 5, 2006, 22:51:02  
 Job time : 20 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 22:46:01 ; Search time 50 Seconds  
(Without alignments)  
33.262 Million cell updates/sec

Title: US-09-403-440A-2  
Perfect score: 105  
Sequence: 1 PPLSQFTFSDMLKLPENG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /EMC\_Celerra\_SIDS3/Plodata/2/1aa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/Plodata/2/1aa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/Plodata/2/1aa/H\_COMB.pep:\*  
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6: /EMC\_Celerra\_SIDS3/Plodata/2/1aa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/Plodata/2/1aa/Backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	94.3	20	2	US-09-081-975-8
2	99	94.3	20	2	US-09-081-975-10
3	99	94.3	20	2	US-09-081-975-11
4	99	94.3	20	2	US-09-081-975-16
5	99	94.3	32	2	US-09-069-827A-48
6	99	94.3	32	2	US-09-958-163A-3
7	99	94.3	64	1	US-08-245-500A-1
8	99	94.3	64	1	US-08-390-546-1
9	99	94.3	64	1	US-08-390-479A-1
10	99	94.3	64	1	US-08-557-393-1
11	99	94.3	64	1	US-08-390-516C-1
12	99	94.3	64	1	US-08-390-517A-1
13	99	94.3	64	1	US-08-390-515A-1
14	99	94.3	64	1	US-08-801-718-1
15	99	94.3	64	2	US-09-170-159A-1
16	99	94.3	261	2	US-09-414-436-3
17	99	94.3	353	2	US-09-849-602-24
18	99	94.3	362	2	US-09-603-052-2
19	99	94.3	363	1	US-08-697-221-17
20	99	94.3	363	1	US-08-697-221-18
21	99	94.3	363	1	US-08-697-221-19
22	99	94.3	363	1	US-08-697-221-20
23	99	94.3	363	1	US-08-697-221-21
24	99	94.3	363	1	US-08-697-221-22
25	99	94.3	363	1	US-08-697-221-23
26	99	94.3	363	1	US-08-697-221-24

27	99	94.3	393	1	US-08-047-041A-25	Sequence 25, App1
28	99	94.3	393	1	US-08-047-041A-26	Sequence 26, App1
29	99	94.3	393	1	US-08-047-041A-27	Sequence 27, App1
30	99	94.3	393	1	US-08-047-041A-28	Sequence 28, App1
31	99	94.3	393	1	US-08-347-792-2	Sequence 2, App1
32	99	94.3	393	1	US-08-390-516C-6	Sequence 6, App1
33	99	94.3	393	1	US-08-390-516C-7	Sequence 7, App1
34	99	94.3	393	1	US-08-390-516C-8	Sequence 8, App1
35	99	94.3	393	1	US-08-390-516C-9	Sequence 9, App1
36	99	94.3	393	1	US-08-431-357-2	Sequence 2, App1
37	99	94.3	393	1	US-08-390-515A-6	Sequence 6, App1
38	99	94.3	393	1	US-08-390-515A-7	Sequence 7, App1
39	99	94.3	393	1	US-08-390-515A-8	Sequence 8, App1
40	99	94.3	393	1	US-08-390-515A-9	Sequence 9, App1
41	99	94.3	393	1	US-08-795-006A-132	Sequence 32, App1
42	99	94.3	393	1	US-08-697-221-2	Sequence 2, App1
43	99	94.3	393	1	US-08-697-221-3	Sequence 3, App1
44	99	94.3	393	1	US-08-697-221-4	Sequence 4, App1
45	99	94.3	393	1	US-08-697-221-11	Sequence 11, App1

## ALIGNMENTS

RESULT 1  
US-09-081-975-8  
Sequence 8, Application US/09081975  
Patent No. 6451979  
GENERAL INFORMATION:  
APPLICANT: Kaelin, William  
TITLE OF INVENTION: METHODS OF TREATMENT USING  
TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon Peabody LLP  
STREET: 101 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,975  
FILING DATE: 12-MAY-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/046,207  
FILING DATE: 12-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-081-975-8  
Query Match 94.3%; Score 99; DB 2; Length 20;  
Best local Similarity 100.0%; Pred. No. 4.3e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSQETPSDLMKLPEN 18  
| | | | | | | | | | | | | | | | | |  
DB 2 PLSQETPSDLMKLPEN 19

## RESULT 2

US-09-081-975-10  
; Sequence 10, Application US/09081975  
; Patent No. 6451979  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; APPLICANT: Jost, Christine  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon Peabody LLP  
; STREET: 101 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/081,975  
; FILING DATE: 12-MAY-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/046,207  
; FILING DATE: 12-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Eisenstein, Ronald I  
; REGISTRATION NUMBER: 30,628  
; REFERENCE/DOCKET NUMBER: 47400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-6054  
; TELEFAX: 617-345-1300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-081-975-10  
Query Match 94.3%; Score 99; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.3e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PLSQETPSDLMKLPEN 18  
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DB 2 PLSQETPSDLMKLPEN 19

## RESULT 3

US-09-081-975-11  
; Sequence 11, Application US/09081975  
; Patent No. 6451979  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; APPLICANT: Jost, Christine  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon Peabody LLP  
STREET: 101 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,975  
FILING DATE: 12-MAY-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/046,207  
FILING DATE: 12-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-081-975-11

Query Match 94.3%; Score 99; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.3e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSQETPSDLMKLPEN 18  
| | | | | | | | | | | | | | | | | |  
DB 2 PLSQETPSDLMKLPEN 19

## RESULT 4

US-09-081-975-16  
; Sequence 16, Application US/09081975  
; Patent No. 6451979  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; APPLICANT: Jost, Christine  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon Peabody LLP  
; STREET: 101 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/081,975  
; FILING DATE: 12-MAY-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/046,207  
; FILING DATE: 12-MAY-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-081-975-16

Query Match 94.3%; Score 99; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.3e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDDLWKLPEN 18  
|||  
Db 2 PPLSQETFSDDLWKLPEN 19

RESULT 5  
US-09-069-827A-48  
Sequence 48, Application US/09069827A  
Patent No. 6617114  
GENERAL INFORMATION:  
APPLICANT: FOWLKES, Dana M  
KAY, Brian K  
PRELINGER, Jeffrey A  
HYDE-DEKUSCHER, Robin P  
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING  
COMPLEMENTARY COMBINATORIAL LIBRARIES  
NUMBER OF SEQUENCES: 178  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROMIDY AND NEIMARK, P.L.L.C.  
STREET: 624 Ninth Street N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/069,827A  
FILING DATE: 30-Apr-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/050,359  
FILING DATE: 31-MAR-1998  
APPLICATION NUMBER: PCT/US97/19638  
FILING DATE: 31-OCT-1997  
APPLICATION NUMBER: US 08/740,671  
FILING DATE: 31-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, Iyer P  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: FOWLKES-4C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 48:  
US-09-069-827A-48

Query Match 94.3%; Score 99; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 7.1e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDDLWKLPEN 18  
|||  
Db 12 PPLSQETFSDDLWKLPEN 29

RESULT 6  
US-09-958-163A-3  
Sequence 3, Application US/09958163A  
Patent No. 6831071  
GENERAL INFORMATION:  
APPLICANT: Sergeev, Pavel  
TITLE OF INVENTION: Synthesis of biologically active compounds in cells  
FILE REFERENCE: sergeev  
CURRENT APPLICATION NUMBER: US/09/958,163A  
CURRENT FILING DATE: 2001-10-03  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3  
LENGTH: 32  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: part of the amino acid sequence of the Human tumour suppressor p53  
PUBLICATION INFORMATION:  
AUTHORS: Harlow, E., Williamson, N.M., Ralston, R., Helfman, D.M. and  
AUTHORS: Adams, T.E.  
TITLE: Molecular cloning and in vitro expression of a cDNA clone for  
TITLE: human cellular tumor antigen p53  
JOURNAL: Molecular and cellular biology  
VOLUME: 5  
ISSUE: 7  
PAGES: 1601-1610  
DATE: 1985-07-01  
DATABASE ACCESSION NUMBER: K03199  
DATABASE ENTRY DATE: 1995-01-07  
US-09-958-163A-3

Query Match 94.3%; Score 99; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 7.1e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDDLWKLPEN 18  
|||  
Db 12 PPLSQETFSDDLWKLPEN 29

RESULT 7  
US-08-245-500A-1  
Sequence 1, Application US/08245500A  
Patent No. 5550023  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILBE  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/245,500A  
FILING DATE: 07-APR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BBMB UT  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 64 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17q  
US-08-245-500A-1

Query Match 94.3%; Score 99; DB 1; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSOETPSDLWKLPEN 18  
DB 12 PPLSOETPSDLWKLPEN 29

RESULT 8  
US-08-390-546-1  
Sequence 1, Application US/08390546  
Patent No. 5606044  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,546  
FILING DATE: 07-APR-1993  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BBMB UT  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 64 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17q  
US-08-390-546-1

Query Match 94.3%; Score 99; DB 1; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSOETPSDLWKLPEN 18  
DB 12 PPLSOETPSDLWKLPEN 29

RESULT 9  
US-08-390-479A-1  
Sequence 1, Application US/08390479A  
Patent No. 5618921  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER & WITCOFF, LTD.  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,479A  
FILING DATE: 02-FEB-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.48992  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BBMB UT  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 64 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17q  
US-08-390-479A-1

Query Match 94.3%; Score 99; DB 1; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLPEN 18  
DB 12 PPLSQETFSDLWKLPEN 29

## RESULT 10

US-08-557-393-1  
Sequence 1, Application US/08557393  
Patent No. 5702903  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/557,393  
FILING DATE: 13-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/245,500  
FILING DATE: 18-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107,42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BBMB UT  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 64 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17q  
US-08-557-393-1

Query Match 94.3%; Score 99; DB 1; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLPEN 18  
DB 12 PPLSQETFSDLWKLPEN 29

## RESULT 11

US-08-390-516C-1  
Sequence 1, Application US/08390516C  
Patent No. 5708136  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,516C  
FILING DATE: 07-APR-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107,42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BBMB UT  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 64 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17q  
US-08-390-516C-1

Query Match 94.3%; Score 99; DB 1; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLPEN 18  
DB 12 PPLSQETFSDLWKLPEN 29

## RESULT 12

US-08-390-517A-1  
Sequence 1, Application US/08390517A

```

Patent No. 5736338
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BEET
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,517A
FILING DATE: 07-APR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BEMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17q
US-08-390-517A-1
Query Match 94.3% Score 99; DB 1; Length 64
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
QY 1 PPLSGTFSDMLKLPEN 18
Db 12 PPLSGTFSDMLKLPEN 29
RESULT 13
US-08-390-515A-1
Sequence 1, Application US/08390515A
Patent No. 5756455
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BEET
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.

```

```

      CITY: WASHINGTON
      STATE: D. C.
      COUNTRY: USA
      ZIP: 20001

      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent in Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/390,515A
      FILING DATE: 07-APR-1993
      CLASSIFICATION: 514
      ATTORNEY/AGENT INFORMATION:
      NAME: KAGAN, SARAH A.
      REGISTRATION NUMBER: 32,141
      REFERENCE/DOCKET NUMBER: 01107.42798
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 202-508-9100
      TELEFAX: 202-508-9299
      TELEX: 197430 BMB UT
      INFORMATION FOR SEQ ID NO: 1:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 64 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      HYPOTHEetical: NO
      ANTI-SENSE: NO
      FRAGMENT TYPE: N-terminal
      ORIGINAL SOURCE:
      ORGANISM: Homo sapiens
      POSITION IN GENOME:
      CHROMOSOME/SEGMENT: 17q
      US-08-390-515A-1

      Query Match          94.3%; Score 99; DB 1; Length 64;
      Best Local Similarity 100.0%; Pred. No. 1.5e-08;
      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      Oy      1 PPLSQETFSIDMKLIPEN 18
              |||||
      Db      12 PPLSQETFSIDMKLIPEN 29

      RESULT 14
      US-08-801-718-1
      ; Sequence 1, Application US/08801718
      ; Patent No. 5858976
      ; GENERAL INFORMATION:
      ; APPLICANT: BURRELL, MARILEE
      ; APPLICANT: HILL, DAVID E.
      ; APPLICANT: KINZLER, KENNETH W.
      ; APPLICANT: VOGELSTEIN, BERT
      ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
      ; TITLE OF INVENTION: HUMAN TUMORS
      ; NUMBER OF SEQUENCES: 9
      ; CORRESPONDENCE ADDRESS:
      ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
      ; STREET: 1001 G STREET, N.W.
      ; CITY: WASHINGTON
      ; STATE: D. C.
      ; COUNTRY: USA
      ; ZIP: 20001

      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent in Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/801,718
      FILING DATE: 14-FEB-1997
  
```

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/390,515  
FILING DATE: 07-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BBMB UT  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 64 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17q  
US-08-801-718-1

Query Match 94.3%; Score 99; DB 1; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDDLWKLPEN 18  
Db 12 PPLSQETFSDDLWKLPEN 29

RESULT 15  
US-09-170-159A-1  
Sequence 1, Application US/09170159A  
Patent No. 6399755  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
HILL, DAVID E.  
KINZLER, KENNETH W.  
VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
HUMAN TUMORS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/170,159A  
FILING DATE: 13-Oct-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 64 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17q  
US-09-170-159A-1

Query Match 94.3%; Score 99; DB 2; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDDLWKLPEN 18  
Db 12 PPLSQETFSDDLWKLPEN 29

Search completed: July 5, 2006, 22:47:26  
Job time: 51 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 5, 2006, 22:54:41 ; Search time 38 Seconds  
(without alignments)  
48.108 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105  
Sequence: 1 PPLSQETFSDDLWKLPENG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3436

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR 80:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	32.4	19	2	B61409 genome polyprotein
2	26	24.8	18	2	A59396 Tha p 1 - Thaumeto
3	25	23.8	14	2	A35105 hypochelical prote
4	25	23.8	15	2	PA0110 translation elonga
5	24	22.9	10	2	A31571 hypetrrehalosemic/
6	24	22.9	11	2	S41747 chaperonin 10 homo
7	23	21.9	8	2	S11545 adipokinetic hormo
8	23	21.9	9	2	A24244 adipokinetic hormo
9	23	21.9	15	2	S20410 protein kinase (EC
10	22	21.0	5	2	S70615 endo-1,4-beta-xyla
11	22	21.0	8	2	S16324 hypochelical prote
12	22	21.0	13	2	S32471 lymnadFamide 1 - 9
13	22	21.0	13	2	S32472 lymnadFamide 2 - 9
14	22	21.0	13	2	S32474 lymnadFamide 4 - 9
15	22	21.0	13	2	S32475 lymnadFamide 5 - 9
16	22	21.0	14	2	B44854 l-2,4-diaminobuty
17	22	21.0	16	2	JH0517 insulin-like growt
18	22	21.0	17	2	S59481 hydroxyproline-ric
19	21.5	20.5	14	2	PH1625 Ig H chain V-D-J r
20	21.5	20.5	15	2	PH1788 T cell receptor al
21	21.5	20.5	18	2	I40062 shikimate 5-dehydr
22	21	20.0	8	2	B44960 neuropeptide led-C
23	21	20.0	8	2	S08996 hypertrehalosemic
24	21	20.0	8	2	B49823 adipokinetic hormo
25	21	20.0	10	2	UC1416 hypertrehalosemic
26	21	20.0	10	2	S09138 hypertrehalosemic
27	21	20.0	10	2	S53789 neuropeptide Pec-H
28	21	20.0	11	2	F33098 214k exantigen (v
29	21	20.0	11	2	S53436 beta-D-galactosida

30	21	20.0	13	2	A35245 histone H1a - mou
31	21	20.0	13	2	B35245 histone H1.c - mou
32	21	20.0	13	2	B56864 dipeptidyl-peptida
33	21	20.0	15	2	A45103 7 alpha-hydroxy-4-
34	21	20.0	15	2	A35389 urease (EC 3.5.1.5
35	21	20.0	16	2	E58503 superoxide dismuta
36	21	20.0	17	2	S15754 actin 6 - soybean
37	21	20.0	18	2	A35704 cytochrome P450 ol
38	21	20.0	19	2	I49037 TCR delta chain V-
39	20.5	19.5	13	2	PC4391 cysteine proteinas
40	20.5	19.5	14	2	PH1627 Ig H chain V-D-J r
41	20.5	19.5	18	2	I52623 hypochelical prote
42	20	19.0	8	2	A33895 adipokinetic hormo
43	20	19.0	8	2	A44960 neuropeptide led-C
44	20	19.0	8	2	S08995 hypertrehalosemic
45	20	19.0	8	2	A49823 adipokinetic hormo

#### ALIGNMENTS

##### RESULT 1

B61409 genome polyprotein (Clone L3/S2) - Skalica virus (fragment)  
C/Species: Skalica virus  
C/Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 31-Dec-2004  
C/Accession: B61409  
R/Guilakho, F.; Heinz, F.X.; Mandl, C.W.; Holzmann, H.; Kunz, C.; Grieskova, M.  
J. Gen. Virol. 72, 333-338, 1991  
A/Title: The relationship between the flaviviruses Skalica and Langat as revealed by mo  
A/Reference number: A61409; PMID:9112129; PMID:1647173  
A/Status: preliminary; not compared with conceptual translation  
A/Accession: B61409  
A/Molecule type: genomic RNA  
A/Residues: 1-19 <GUI>  
A/Cross-references: UNIPROT:Q7LZY3; UNIPARC:UPI0000174A0E  
C/Superfamily: Hepatitis C virus genome polyprotein

##### Query Match

Best Local Similarity 32.4%; Score 34; DB 2; Length 19;  
Best Local Similarity 41.7%; Pred. No. 84;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 PPLSQETFSDDLW 12  
||:|:|:|:|:|

DB 2 PPVYRTGTDCW 13

##### RESULT 2

A59396 Tha p 1 - Thaumetopoea pityocampa (fragment)  
C/Species: Thaumetopoea pityocampa  
C/Date: 03-Jun-2002 #sequence\_revision 03-Jun-2002 #text\_change 09-Jul-2004  
C/Accession: A59396  
R/Mone, I.  
submitted to the Protein Sequence Database, September 2001

A/Description: Isolation and characterization of a major allergen of the pine procession

A/Reference number: A59396

A/Accession: A59396

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-18 <MON>

A/Cross-references: UNIPROT:Q7MK48; UNIPARC:UPI000017CD37

A/Experimental source: L5

A/Note: IGE-binding protein, major allergen

Query Match 24.8%; Score 26; DB 2; Length 18;

Best Local Similarity 38.5%; Pred. No. 13e+03; Mismatches 5; Indels 0; Gaps 0;

QY 6 ETFSDLMKLPEN 18  
||:|:|:|:|:|

DB 2 ETVSDKVTIDVN 14

## RESULT 3

AS105  
hypothetical protein - Neurospora crassa mitochondrion (fragment)  
C:Species: mitochondrion Neurospora crassa  
C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 07-Dec-1999  
C:Accession: A35105  
R:Saville, B.J.; Collins, R.A.  
Cell 61, 685-696, 1990  
A>Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora m  
A:Reference number: A35105; MUID:90263093; PMID:2160856  
A:Accession: A35105  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-14 <SAV>  
A:Cross-references: UNIPARC:UPI000017B520  
C:Genetics:  
A:Genome: mitochondrion  
A:Genetic code: SGC3  
C:Keywords: mitochondrion

Query Match 23.8%; Score 25; DB 2; Length 14;  
Best Local Similarity 54.5%; Pred. No. 1.4e+03;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 9 SLMKLLPENG 19  
DB 2 SFLMTLLQK 12

## RESULT 4

PA010  
translation elongation factor eEF-1 beta' chain - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 07-Apr-1995 #sequence\_revision 26-May-1995 #text\_change 31-Dec-2004  
C:Accession: PA0110  
R:Kamo, M.; Kawakami, T.; Tsugita, A.  
submitted to JIPID, March 1995  
A:Reference number: PA0109  
A:Accession: PA0110  
A:Molecule type: protein  
A:Residues: 1-15 <KME>  
A:Cross-references: UNIPROT:Q9SCX3; UNIPARC:UPI000017B01C  
C:Superfamily: translation elongation factor eEF-1 beta chain

Query Match 23.8%; Score 25; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TFSDL 11  
DB 3 TFSDL 7

## RESULT 5

A31571  
hypertrehalosemic/adipokinetic hormone - bollworm  
N:Alternate names: Hez-HTH  
C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)  
C>Date: 30-Jun-1989 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C:Accession: A31571  
R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.  
Biochem. Biophys. Res. Commun. 155, 344-350, 1988  
A>Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea wi  
A:Reference number: A31571; MUID:88326324; PMID:3415690  
A:Accession: A31571  
A:Molecule type: protein  
A:Residues: 1-10 <JAF>

A:Cross-references: UNIPROT:P16353; UNIPARC:UPI000012CDC5  
C:Superfamily: adipokinetic hormone  
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:10/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 22.9%; Score 24; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.4e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETFSDLW 12  
DB 1 QUTFSSGW 8

## RESULT 6

S41747  
chaperonin 10 homolog - potato (fragment)  
C:Species: Solanum tuberosum (potato)  
C>Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: S41747  
R:Butt, W.J.E.; Weaver, C.J.  
FEBS Lett. 339, 139-141, 1994  
A>Title: Identification of a chaperonin-10 homologue in plant mitochondria.  
A:Reference number: S41747; MUID:94148071; PMID:7906228  
A:Accession: S41747  
A:Molecule type: protein  
A:Residues: 1-11 <BUR>  
A:Cross-references: UNIPROT:Q7MH1; UNIPARC:UPI000017B0B8  
A:Experimental source: mitochondrion  
C:Keywords: mitochondrion; molecular chaperone

Query Match 22.9%; Score 24; DB 2; Length 11;  
Best Local Similarity 83.3%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 LLPENG 19  
DB 2 LLPENG 7

## RESULT 7

S11545  
adipokinetic hormone - nestling-sucking blowfly  
C:Species: Protophormia terraenovae (nestling-sucking blowfly)  
C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C:Accession: S11545  
R:Gaede, G.; Wilps, H.; Kellner, R.  
Biochem. J. 269, 309-313, 1990  
A>Title: Isolation and structure of a novel charged member of the red-pigment-concentra  
extraenova (Diptera).  
A:Reference number: S11545; MUID:90351345; PMID:2386478  
A:Accession: S11545  
A:Molecule type: protein  
A:Residues: 1-8 <GAE>  
A:Cross-references: UNIPROT:P61856; UNIPARC:UPI00001734FA  
C:Superfamily: adipokinetic hormone  
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 21.9%; Score 23; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. No. 2.8e+05;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETFSDLW 12  
DB 1 QUTFSPDW 8

## RESULT 8

A24244  
adipokinetic hormone - bollworm  
N:Alternate names: Hez-AKH  
C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)  
C>Date: 31-Mar-1988 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C:Accession: A24244  
R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgwa

Biochem. Biophys. Res. Commun. 135, 622-628, 1986  
A/Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helix  
A/Reference number: A24244; MUID:86186794; PMID:3964263  
A/Accession: A24244  
A/Molecule type: protein  
A/Residues: 1-9 <JAF>  
A/Cross-references: UNIPROT: P08901; UNIPARC: UP1000017661D  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F/1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
F/9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 21.9%; Score 23; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETFSDLW 12  
| | | | |  
| | | | |  
Db 1 QLFTSSW 8

RESULT 9  
S20410  
protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)  
N/Alternate names: LHCI protein kinase  
C/Species: chloroplast Spinacia oleracea (spinach)  
C/Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C/Accession: S20410  
R/Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.  
FEBS Lett. 298, 33-35, 1992  
A/Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cyto  
A/Reference number: S20410; MUID:92183823; PMID:1544419  
A/Accession: S20410  
A/Molecule type: protein  
A/Residues: 1-15 <GAL>  
A/Cross-references: UNIPROT: Q9T2K8; UNIPARC: UP1000008540D  
C/Genetics:  
A/Genome: chloroplast  
C/Function:  
A/Description: is responsible for the regulation of energy distribution between photosys  
A/Note: does not exhibit redox-controlled activation  
C/Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phospho

Query Match 21.9%; Score 23; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 3e+03;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PPLSOTFSD 10  
| | | | |  
| | | | |  
Db 5 PDVEKSTLSD 14

RESULT 10  
S70615  
endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (fragment  
N/Alternate names: xylanase  
C/Species: Streptomyces sp.  
A/Variety: Chainia sp. NCL 82.5.1  
C/Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999  
C/Accession: S70615  
R/Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.  
Biochem. J. 316, 771-775, 1996  
A/Title: Structural environment of an essential cysteine residue of xylanase from Chaini  
A/Reference number: S70615; MUID:96265041; PMID:8670151  
A/Accession: S70615  
A/Molecule type: protein  
A/Residues: 1-5 <RAO>  
A/Cross-references: UNIPARC: UP1000017AB36  
A/Experimental source: Chainia sp. strain NCL 82.5.1  
A/Note: the source is designated as Chainia sp.  
C/Function:  
A/Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans  
A/Pathway: fermentation of hemicellulose into ethanol

C/Keywords: glycosidase; hydrolase

Query Match 21.0%; Score 22; DB 2; Length 5;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ETFSD 10  
| | | | |  
| | | | |  
Db 1 ETFXD 5

RESULT 11  
S16324  
hypothetical protein 2 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 21-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 21-Jul-2000  
C/Accession: S16324  
R/Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.  
EMBO J. 10, 1787-1791, 1991  
A/Title: A novel class of plant proteins containing a homeodomain with a closely linked  
A/Reference number: S16323; MUID:91266907; PMID:1675603  
A/Accession: S16324  
A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-8 <RUB>  
A/Cross-references: UNIPARC: UP1000011DF52; EMBL: X58821; NID: G16327; PIDN: CAA41624.1; PI

Query Match 21.0%; Score 22; DB 2; Length 8;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 WKLP 16  
| | | | |  
| | | | |  
Db 3 YKLP 7

RESULT 12  
S32471  
LymadPamide 1 - great pond snail  
C/Species: Lymnaea stagnalis (great pond snail)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S32471  
R/Johnsen, A.H.; Rehfeld, J.F.  
Eur. J. Biochem. 213, 875-879, 1993  
A/Title: LymadPamides, a new family of neuropeptides from the pond snail, Lymnaea stag  
A/Reference number: S32471; MUID:93238777; PMID:8477756  
A/Accession: S32471  
A/Molecule type: protein  
A/Residues: 1-13 <JOH>  
A/Cross-references: UNIPROT: P80178; UNIPARC: UP100001303C5; PIDN: AAB26362.1; PID: G299829  
A/Experimental source: ganglia  
C/Keywords: amidated carboxyl end; neuropeptide  
F/13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 21.0%; Score 22; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.6e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSOETPSD 10  
| | | | |  
| | | | |  
Db 5 ISNSAFSD 12

RESULT 13  
S32472  
LymadPamide 2 - great pond snail  
C/Species: Lymnaea stagnalis (great pond snail)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S32472  
R/Johnsen, A.H.; Rehfeld, J.F.  
Eur. J. Biochem. 213, 875-879, 1993  
A/Title: LymadPamides, a new family of neuropeptides from the pond snail, Lymnaea stag  
A/Reference number: S32471; MUID:93238777; PMID:8477756

A:Accession: S32472  
A:Molecule type: protein  
A:Residues: 1-13 <JOH>  
A:Cross-references: UNIPROT:P60181; UNIPARC:UPI00001303CA; PIDN:AAE26363.1; PID:G299830  
A:Experimental source: ganglia  
C:Keywords: amidated carboxyl end; neuropeptide  
F:13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 21.0%; Score 22; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.6e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSOETFSFSD 10  
: | |||  
Db 5 ISSSAFSD 12

## RESULT 14

S32474  
LymnadFamide 4 - great pond snail  
C:Species: Lymnaea stagnalis (great pond snail)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S32474  
R:Johnsen, A.H.; Rehfeld, J.F.  
Eur. J. Biochem. 213, 875-879, 1993  
A:Title: LymnadFamides, a new family of neuropeptides from the pond snail, Lymnaea stagnalis  
A:Reference number: S32471; MVID:93238777; PMID:8477756  
A:Accession: S32474  
A:Molecule type: protein  
A:Residues: 1-13 <JOH>  
A:Cross-references: UNIPROT:P60181; UNIPARC:UPI00001303D0; PIDN:AAE26365.1; PID:G299832  
A:Experimental source: ganglia  
C:Keywords: amidated carboxyl end; neuropeptide  
F:13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 21.0%; Score 22; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.6e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSOETFSFSD 10  
: | |||  
Db 5 ISSSAFSD 12

## RESULT 15

S32475  
LymnadFamide 5 - great pond snail  
C:Species: Lymnaea stagnalis (great pond snail)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S32475  
R:Johnsen, A.H.; Rehfeld, J.F.  
Eur. J. Biochem. 213, 875-879, 1993  
A:Title: LymnadFamides, a new family of neuropeptides from the pond snail, Lymnaea stagnalis  
A:Reference number: S32471; MVID:93238777; PMID:8477756  
A:Accession: S32475  
A:Molecule type: protein  
A:Residues: 1-13 <JOH>  
A:Cross-references: UNIPROT:P60182; UNIPARC:UPI00001303D2; PIDN:AAE26366.1; PID:G299833  
A:Experimental source: ganglia  
C:Keywords: amidated carboxyl end; neuropeptide  
F:13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 21.0%; Score 22; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.6e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSOETFSFSD 10  
: | |||  
Db 5 ISSSAFSD 12

Search completed: July 5, 2006, 23:00:04  
Job time : 39 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 5, 2006, 22:51:16 ; Search time 293 Seconds

(Without alignments)  
59.984 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSFLMKLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 14129

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	32.4	19	2	Q7LZY3_9FLAV
2	32	30.5	19	2	CRTC_ENTHI
3	31	29.5	16	2	Q9BG68_SORAR
4	29	27.6	14	2	Q6SE52_DROSI
5	29	27.6	17	2	Q9XN01_BOOMI
6	28	26.7	15	2	Q6LC27_HUMAN
7	28	26.7	19	2	Q5SR29_MOUSE
8	27.5	26.2	18	2	Q2QKX4_9HEMI
9	27.5	26.2	11	2	Q2QKX1_9HEMI
10	27	25.7	11	2	Q9UEI0_HUMAN
11	27	25.7	14	2	Q71H30_9HYME
12	27	25.7	19	2	Q6LD35_RAT
13	26	24.8	14	2	P82326_PEA
14	26	24.8	17	2	Q9UJZ3_HUMAN
15	26	24.8	18	2	Q9UJZ3_HUMAN
16	26	24.8	18	2	Q7MAK8_9NEOP
17	26	24.8	19	2	Q7SE65_NEUCP
18	25	23.8	16	2	Q83960_9INFA
19	25	23.8	17	2	Q9F0P3_PARDE
20	25	23.8	18	2	Q8NFB4_HUMAN
21	25	23.8	18	2	P82674_BOVIN
22	25	23.8	18	2	Q84129_9INFA
23	25	23.8	19	2	Q22064_9LILI
24	25	23.8	19	2	Q83965_9INFA
25	24	22.9	9	2	Q7HE72_RAT
26	24	22.9	10	1	HTF_HEITZ
27	24	22.9	10	2	Q9M05_PODCU
28	24	22.9	10	2	Q9ESU5_MOUSE
29	24	22.9	11	2	Q7M1H1_SOLTU
30	24	22.9	12	1	CU28A_LACCU
31	24	22.9	12	2	Q77919_9CICH

32	24	22.9	14	2	Q9MJQ3_PODCU	Q9MJQ3_PODCU
33	24	22.9	15	2	Q6LCW3_MOUSE	Q6LCW3_MOUSE
34	24	22.9	15	2	Q9PS10_CHICK	Q9PS10_CHICK
35	24	22.9	16	2	Q83967_9INFA	Q83967_9INFA
36	24	22.9	16	2	Q84055_9INFA	Q84055_9INFA
37	24	22.9	17	2	Q9QVS6_9MURI	Q9QVS6_9MURI
38	23.5	22.4	18	2	Q2QKX8_9HEMI	Q2QKX8_9HEMI
39	23.5	22.4	18	2	Q2QKX0_9HEMI	Q2QKX0_9HEMI
40	23.5	22.4	18	2	Q2QKX2_9HEMI	Q2QKX2_9HEMI
41	23.5	22.4	18	2	Q2QKX7_9HEMI	Q2QKX7_9HEMI
42	23.5	22.4	18	2	Q2QKX9_9HEMI	Q2QKX9_9HEMI
43	23.5	22.4	18	2	Q2QKX5_9HEMI	Q2QKX5_9HEMI
44	23.5	22.4	18	2	Q2QKX9_9HEMI	Q2QKX9_9HEMI
45	23.5	22.4	18	2	Q2QKX1_9HEMI	Q2QKX1_9HEMI

## ALIGNMENTS

```

RESULT 1
Q7LZY3_9FLAV          PRELIMINARY;  PRT;   19 AA.
ID   Q7LZY3_9FLAV
AC   Q7LZY3;
DT   15-DEC-2003, integrated into UniProtKB/TREMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Genome polypeptide (Clone L3/S2) (Fragment).
OS   Skallia virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC   Flavivirus; tick-borne encephalitis virus group.
OX   NCBI_TaxID=37555;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Guitrakho F., Heinz F.X., Mandl C.W., Holzmann H., Kunz C.,
RA   Grestikova M.;
RT   "The relationship between the flaviviruses Skallia and Langat as
RT   revealed by monoclonal antibodies, peptide mapping and RNA sequence
RT   analysis."
RL   J. Gen. Virol. 72:333-338(1991).
RN   [2]
RP   MEDLINE SEQUENCE.
RX   MEDLINE=91132129; PubMed=1847173;
RA   Guitrakho F., Heinz F.X., Mandl C.W., Holzmann H., Kunz C.,
RA   Grestikova M.;
RT   "The relationship between the flaviviruses Skallia and Langat as
RT   revealed by monoclonal antibodies, peptide mapping and RNA sequence
RT   analysis."
RL   J. Gen. Virol. 72:333-338(1991).
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DR   PIR; B61409; B61409.
DR   InterPro; IPR001157; Flavi_NSI.
DR   Pfam; PF00948; Flavi_NSI; 1.
DR   ProDom; PD001496; Flavi_NSI; 1.
FT   NON_TER
FT   NON_TER
SQ   SEQUENCE   19 AA;  2273 MW;  34341CA79E1F7E38 CRC64;

Query Match          32.4%;  Score 34;  DB 2;  Length 19;
Best Local Similarity 41.7%;  Pred. No. 9e+02;
Matches 5;  Conservative 3;  Mismatches 4;  Indels 0;  Gaps 0;

QY   1 PPLSQETFSFLMW 12
    ||: ||: ||
Db    2 PPTVTRGTDCW 13

RESULT 2
CRTC_ENTHI
ID   CRTC_ENTHI          STANDARD;  PRT;   19 AA.
AC   P83003;

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DT 04-JAN-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2001, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Calreticulin (Fragment).
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=12518855;
RA Gonzalez E., Risco G., Mendoza G., Ramos F., Garcia G., Moran P.,
  Valdez A., Melendo E.I., Ximenez C.;
RT "Calreticulin-like molecule in trophozoites of Entamoeba histolytica
  HM1:IMSS (SwissProt: accession P83003).";
RL Am. J. Trop. Med. Hyg. 67:636-639(2002).
CC -!- FUNCTION: Molecular calcium binding chaperone promoting folding,
  oligomeric assembly and quality control in the ER via the
  calreticulin/calnexin cycle. This lectin may interact transiently
  with almost all of the monoglucosylated glycoproteins that are
  synthesized in the ER (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -!- SIMILARITY: Belongs to the calreticulin family.
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CC -----
DR GO: GO:0005829; C:cytosol; ISS.
DR GO: GO:0005788; C:endoplasmic reticulum lumen; ISS.
DR GO: GO:0005509; F:calcium ion binding; ISS.
DR GO: GO:0003677; F:DNA binding; ISS.
DR GO: GO:0006874; P:calcium ion homeostasis; ISS.
DR GO: GO:0006611; P:protein-nucleus export; ISS.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
DR InterPro: IPR001580; Calret/calnex.
DR InterPro: IPR000886; ER target S.
DR PROSITE: PS00803; CALRETICULIN_1; PARTIAL.
DR PROSITE: PS00804; CALRETICULIN_2; PARTIAL.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; PARTIAL.
DR PROSITE: PS00014; ER_TARGET; PARTIAL.
DR KEGG: KEGG01045; Calreticulin; Direct protein sequencing; Endoplasmic reticulum;
  Lectin; Metal-binding; zinc.
FT CHAIN 1 >19 Calreticulin.
FT FTID=PRO_0000208521.
FT NON TER 19 19 /FTID=PRO_0000208521.
SQ SEQUENCE 19 AA; 2489 MW; FC90BCAEFE1BA764 CRC64;

Query Match 30.5%; Score 32; DB 1; Length 19;
Best Local Similarity 45.5%; Pred. No. 1.8e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETPSDIWKIL 15
Db 5 EETPENGWKKI 15

RESULT 3
Q9BGG8_SORAR PRELIMINARY; PRT; 16 AA.
AC Q9BGG8;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DE 07-FEB-2006, entry version 9.
DE Thyroid hormone receptor alpha (Fragment).
GN Name=THRA1;
OS Sorex araneus (Eurasian common shrew) (European shrew).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eulestomii;
  Mammalia; Eutheria; Laurasiatheria; Insectivora; Soricidae; Soricinae;
  Sorex.
OX NCBI_TaxID=42254;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Larkin D., Serov O., Zhdanova N.;

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RT "Mapping of five genes from human chromosome 17 to chromosome hn of
  the common shrew (Sorex araneus).";
RL Acta Theriol. 45:143-146(2000).
CC -----
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CC -----
DR EMBL: AF314827; AAK13419.1; -; Genomic DNA.
DR GO: GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1 1
SQ SEQUENCE 16 AA; 1951 MW; 775186E3FE5F52E2 CRC64;

Query Match 29.5%; Score 31; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 PPLSQETPSD 10
Db 4 PPLFLEVFSD 13

RESULT 4
Q6SE52_DROSI PRELIMINARY; PRT; 14 AA.
AC Q6SE52;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 7.
DE Pgi (Fragment).
GN Name=Pgi;
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14762063; DOI=10.1101/gr.1329204;
RA Halligan D.L., Eyre-Walker A., Andolfatto P., Keightley P.D.;
RT "Patterns of evolutionary constraints in intronic and intergenic DNA
  of Drosophila.";
RL Genome Res. 14:273-279(2004).
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CC -----
DR EMBL: AY459549; AAR23007.1; -; Genomic DNA.
DR FlyBase: FBgn0012850; DsIm\Pgi.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1456 MW; 2C83E49CCD8E7E37 CRC64;

Query Match 27.6%; Score 29; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 3.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQE 6
Db 6 PPLNQE 11

RESULT 5
Q9XN01_BOOMI PRELIMINARY; PRT; 17 AA.
AC Q9XN01;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE Cytochrome oxidase subunit 2 (Fragment).
GN Name=COT1;
OS Boophilus microplus (Cattle tick).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

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OC Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=N;
RC MEDLINE=99297341; PubMed=10368952;
RA Campbell N.J.H., Barker S.C.;
RT "The novel mitochondrial gene arrangement of the cattle tick,
  Boophilus microplus: fivefold tandem repetition of a coding region.";
RL Mol. Biol. Evol. 16:732-740(1999).
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CC -----
DR EMBL, AF110614; AAD28397.1; -; Genomic_DNA.
DR GO, GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 17 AA; 1988 MW; 319F2D4DA7DA11F3 CRC64;

Query Match
Best Local Similarity 27.6%; Score 29; DB 2; Length 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SOETFSDL 11
Db 5 SOLTFSDFW 12

RESULT 6
O6LCZ7 HUMAN PRELIMINARY; PRT; 15 AA.
AC O6LCZ7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Interleukin-8 receptor type B (Fragment).
GN Name=IL8RB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RX NUCLEOTIDE SEQUENCE.
RA MEDLINE=95014476; PubMed=7929358;
RA Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
RT "Comparison of the genomic organization and promoter function for
  human interleukin-8 receptors A and B.";
RL J. Biol. Chem. 269:26381-26389(1994).
CC -----
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CC -----
DR EMBL, U11873; AAA64381.1; -; mRNA.
DR EMBL, U11874; AAA64382.1; -; mRNA.
DR EMBL, U11875; AAA64383.1; -; mRNA.
DR EMBL, U11876; AAA64384.1; -; mRNA.
DR EMBL, U11877; AAA64385.1; -; mRNA.
DR EMBL, U11878; AAA64386.1; -; mRNA.
DR EMBL, U11879; AAA64387.1; -; mRNA.
DR GO, GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER
SQ SEQUENCE 15 AA; 1929 MW; 8937AF0B93D4F48C CRC64;

Query Match
Best Local Similarity 26.7%; Score 28; DB 2; Length 15;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 LSOETFSDLW 12
Db 6 MESDSFEDFW 15
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RESULT 7
Q5SR29 MOUSE PRELIMINARY; PRT; 19 AA.
ID Q5SR29;
AC Q5SR29;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hepatic leukemia factor (Fragment).
GN Name=HLF; ORFNames=RP23-220F20.3-004;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Myriodonta; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Skuce C.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL, AL691494; CA124995.1; -; Genomic_DNA.
DR EMBL, ENSMUSG0000003949; Mus musculus.
DR MGI, MGI:96108; Hlf.
FT NON TER
SQ SEQUENCE 19 AA; 2127 MW; 7E9AE981C48DFC24 CRC64;

Query Match
Best Local Similarity 26.7%; Score 28; DB 2; Length 19;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 10 DLWKLPLPENG 19
Db 2 DLSEFLSENG 11

RESULT 8
Q2QKW4 SHEMI PRELIMINARY; PRT; 18 AA.
ID Q2QKW4;
AC Q2QKW4;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 21-FEB-2006, entry version 3.
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Hyadaphis tataricae.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphidoidea; Aphididae; Macrosiphini; Hyadaphis.
OX NCBI_TaxID=330428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16368250;
RA von Dohlen C.D., Rowe C.A., Heie O.E.;
RT "A test of morphological hypotheses for tribal and subtribal
  relationships of Aphidinae (Insecta: Hemiptera: Aphididae) using DNA
  sequences.";
RL Mol. Phylogenet. Evol. 38:316-329(2006).
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CC -----
DR EMBL, DD005174; AAY55999.1; -; Genomic_DNA.
DR GO, GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 18 AA; 2114 MW; B4E9A8EA785E7E4B CRC64;

Query Match
Best Local Similarity 26.2%; Score 27.5; DB 2; Length 18;
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Best Local Similarity 54.5%; Pred. No. 8.3e+03;  
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 PPLSQETFSDL 11  
||| : ||| :  
Db 4 PPL-EHTYSEL 13

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RESULT 9
ID 020KX1_9HEMI PRELIMINARY; PRT; 18 AA.
AC 020KX1.
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DE 21-FEB-2006, entry version 3.
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI.
OS Hyalopteris prunifolia.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphididae; Aphididae; Hyalopteris.
OX NCBI_TaxID=312888;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16368250;
RA von Dohlen C.D., Rowe C.A., Heie O.E.;
RT "A test of morphological hypotheses for tribal and subtribal
RT relationships of Aphidinae (Insecta: Hemiptera: Aphididae) using DNA
RT sequences."
RL Mol. Phylogenet. Evol. 38:316-329(2006).
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CC -----
DR EMBL; DQ005170; AAY5592.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2100 MW; B399A8EA785E7E4B CRC64;

Query Match 26.2%; Score 27.5; DB 2; Length 18;
Best Local Similarity 54.5%; Pred. No. 8.3e+03;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 PPLSQETFSDL 11
||| : ||| :
Db 4 PPL-EHTYSEL 13

RESULT 10
ID 09UELO_HUMAN PRELIMINARY; PRT; 11 AA.
AC 09UELO.
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 12.
DE Fas antigen (CD95 antigen) (Fragment).
GN Name=CD95;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=95355401; PubMed=7543095; DOI=10.1074/jbc.270.30.18007;
RA Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
RA Nakatani Y.;
RT "Transcription stimulation of the Fas-encoding gene by nuclear factor
RT for interleukin-6 expression upon influenza virus infection.";
RL J. Biol. Chem. 270:18007-18012(1995).

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RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Muschen M., Re D., Brauning A., Wolf J., Hansmann M.L., Diehl V.,
RA Koppers R., Rajewsky K.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Koppers R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=24404279; PubMed=12516573;
RX DOI=10.1002/1521-4141(200212)32:12<3785::AID-IMMU3785>3.0.CO;2-E;
RA Kurch J., Pernthor A., Schmitz R., Iking-Konert C., Chlorazzi N.,
RA Thompson K.M., Winkler T., Rajewsky K., Koppers R.;
RT "Lack of deleterious somatic mutations in the CD95 gene of
RT plasmablasts from systemic lupus erythematosus patients and
RT autoantibody-producing cell lines.";
RL Eur. J. Immunol. 32:3785-3792(2002).
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CC -----
DR EMBL; D31968; BAA20850.1; -; Genomic DNA.
DR EMBL; AJ279011; CAC35539.1; -; Genomic DNA.
DR EMBL; AJ279012; CAC35540.1; -; Genomic DNA.
DR EMBL; AJ279013; CAC35541.1; -; Genomic DNA.
DR EMBL; AJ509179; CAD48929.1; -; Genomic DNA.
DR EMBL; AJ509180; CAD48930.1; -; Genomic DNA.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;

Query Match 25.7%; Score 27; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 5.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 LWKLTP 16
: ||| :
Db 4 IWTLLP 9

RESULT 11
ID 071H30_9HYME PRELIMINARY; PRT; 14 AA.
AC 071H30.
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-MAR-2006, entry version 9.
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena braccata.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apoecrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena; Callandrena.
OX NCBI_TaxID=205219;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=128;
RX PubMed=16343953; DOI=10.1016/j.ympev.2005.10.003;
RA Larkin L., Neff J.L., Simpson B.B.;
RT "Phylogeny of the Callandrena subgenus of Andrena (Hymenoptera:
RT Andrenidae) based on mitochondrial and nuclear DNA data: Polyphyly and
RT convergent evolution.";
RL Mol. Phylogenet. Evol. 38:330-343(2006).
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CC -----
DR EMBL; AF504324; AA007619.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1657 MW; FEA179F0E615AFBA CRC64;

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Query Match 25.7%; Score 27; DB 2; Length 14;  
 Best Local Similarity 44.4%; Pred. No. 7.6e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 FSDLMKLLP 16  
 ||:|:  
 1 FTLMLKXTP 9

Db

RESULT 12  
 Q6LD35\_RAT PRELIMINARY; PRT; 19 AA.  
 AC 06LD35\_ RAT  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 6.  
 DE Brain natriuretic peptide (Fragment).  
 GN Name=BNP;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Sprague Dawley;  
 RX MEDLINE=94299479; PubMed=8027030;  
 RA Thuermer D.J., Hanford D.S., Glembocki C.C.;  
 RT "Regulation of rat brain natriuretic peptide transcription. A  
 potential role for GATA-related transcription factors in myocardial  
 cell gene expression.";  
 RU J. Biol. Chem. 269:17772-17775(1994).  
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 CC

DR EMBL: U02972; AAA21648.1; -; Genomic\_DNA.  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2256 MW; 5E3DB548B919F1C4 CRC64;

QY Query Match 25.7%; Score 27; DB 2; Length 19;  
 Best Local Similarity 62.5%; Pred. No. 1.1e+04;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 10 DLWKLPE 17  
 ||:|:  
 2 DLQKVLPG 9

RESULT 13  
 P83326\_PEA PRELIMINARY; PRT; 14 AA.  
 AC P83326;  
 DT 01-JUN-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-JUN-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 14.  
 DE Unknown protein from 2D-page of thylakoid lumen (SPOT107) (Fragment).  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC Rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
 OX NCBI\_TaxID=3886;  
 RN [1]  
 RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;  
 RX MEDLINE=20181728; PubMed=10715320; DOI=10.1105/tpc.12.3.319;  
 RA Belter J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,  
 Adamka I., van Wijk K.J.;  
 RT "Proteomics of the chloroplast: systematic identification and  
 targeting analysis of lumenal and peripheral thylakoid proteins.";  
 RL Plant Cell 12:319-341(2000).  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.

CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 18.3 KDa.  
 CC

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 CC

DR GO: GO:0009507; C:chloroplast; IEA.  
 DR GO: GO:0009579; C:thylakoid; IEA.  
 KW Chloroplast; Thylakoid.  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1580 MW; 314A6CB514E1B237 CRC64;

QY Query Match 24.8%; Score 26; DB 2; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+04;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 PPLSQE 6  
 ||:|:  
 6 PPLSTE 11

RESULT 14  
 Q9QV57\_9MURI PRELIMINARY; PRT; 17 AA.  
 AC Q9QV57;  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 11.  
 DE Lactate dehydrogenase-A (Fragment).  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=95201434; PubMed=7534515;  
 RA Sandilache R., Pretsch W., Chatterjee B., Gimbel W., Graw J.,  
 RA Favor J.;  
 RT "Molecular analysis of four lactate dehydrogenase-A mutants in the  
 RT mouse.";  
 RL Mamm. Genome 5:777-780(1994).  
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 CC

DR EMBL: U02972; AAA21648.1; -; Genomic\_DNA.  
 FT NON\_TER 19  
 SQ SEQUENCE 17 AA; 1982 MW; E941E0A3F2477D45 CRC64;

QY Query Match 24.8%; Score 26; DB 2; Length 17;  
 Best Local Similarity 30.8%; Pred. No. 1.3e+04;  
 Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Db 1 PPLSQE 13  
 ||:|:  
 4 PELGTDHKEQWK 16

RESULT 15  
 Q9UJ23\_HUMAN PRELIMINARY; PRT; 18 AA.  
 AC Q9UJ23;  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE Oviduct glycoprotein (Fragment).  
 GN Name=OGP;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
RA Lee K.F., Kwok K.L., Agarwal A., Lee Y.L.;  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
CC -----  
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CC Distributed under the Creative Commons Attribution-NonDerivs license  
CC -----  
DR EMBL; AF189710; AAF01065.1; -; Genomic DNA.  
DR Ensembl; ENSG00000085465; Homo sapiens.  
FT NON TER 18 18  
SQ SEQUENCE 18 AA; 2201 MW; 5E8FD91EA210E516 CRC64;  
  
Query Match 24.8%; Score 26; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 1.4e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 LWKLL 15  
:||||  
Db 1 MWKLL 5

Search completed: July 5, 2006, 22:59:21  
Job time : 295 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 5, 2006, 22:50:51 ; Search time 192 Seconds  
(without alignments)  
45.245 Million cell updates/sec

Title: US-09-403-440A-2

Sequence: 1 PPLSQETFSDFLWKLPENG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 919705

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq.8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	19	2 AAW82321	Aaw82321 p53 homol
2	105	100.0	19	2 AAW82319	Aaw82319 p53 homol
3	99	94.3	18	2 AAW37228	Aaw37228 p53 N-ter
4	97	92.4	19	2 AAW47074	Aaw47074 p53/RB in
5	95	90.5	19	6 AAE30870	AAe30870 Peptide u
6	92	87.6	19	6 AAE373435	AAg73435 Human p53
7	92	87.6	19	8 ADR20234	Adr20234 Mixed ele
8	88	83.8	16	6 AAE30872	AAe30872 BOX-1 dom
9	85	81.0	16	10 AEF16088	AEf16088 Novel sta
10	81	77.1	15	2 AAY06310	AAy06310 Human p53
11	81	77.1	15	6 AAG75806	AAg75806 Solid pha
12	81	77.1	15	7 ADC22282	Adc22282 Protein b
13	81	77.1	15	8 ADG78883	Adg78883 Human p53
14	81	77.1	15	8 ADN48957	Adn48957 Peptide #
15	81	77.1	15	9 ADQ09921	Adq09921 Pancreati
16	81	77.1	15	9 AED80637	Aed80637 Human p53
17	81	77.1	17	10 AEE74960	Aee74960 p53/MDM2-
18	77	73.3	15	2 AAR54909	Aar54909 Immunodom
19	77	73.3	15	2 AAR54910	Aar54910 Immunodom
20	77	73.3	15	3 AAB89914	Aab89914 p53 prote
21	77	73.3	15	2 AAB29157	Aab29157 Peptide #
22	77	73.3	15	4 AAG89730	Aag89730 p53 DR3 b
23	77	73.3	15	4 AAG89500	Aag89500 p53 DR 3a

24	77	73.3	15	6 AEG73434	ABg73434 Human p53
25	77	73.3	15	8 ADT02875	Adt02875 Human p53
26	77	73.3	17	2 AAY45227	Aay45227 p53 pepet
27	77	73.3	19	6 ABP97122	ABp97122 Human p53
28	75	71.4	16	10 AEF16089	AEf16089 Novel sta
29	74	70.5	14	8 ADU00102	ADu00102 Amino aci
30	74	70.5	15	3 AAB29159	Aab29159 Peptide #
31	74	70.5	15	3 AAB29163	Aab29163 Peptide #
32	74	70.5	18	8 ADT79028	Adt79028 Mouse p53
33	73	69.5	13	9 ADZ38449	Adz38449 Human kin
34	73	69.5	14	5 ABB05528	ABb05528 Biotinyla
35	73	69.5	15	3 AAB29167	Aab29167 Peptide #
36	73	69.5	15	6 AAE30860	AAe30860 EGFP-S20D
37	73	69.5	15	8 ADT78973	Adt78973 Human p53
38	73	69.5	16	10 AEF16090	AEf16090 Novel sta
39	71	67.6	15	3 AAY99001	Aay99001 HLA Class
40	71	67.6	15	3 AAB29161	Aab29161 Peptide #
41	71	67.6	15	3 AAB29160	Aab29160 Peptide #
42	70	66.7	13	3 AAY57799	Aay57799 TRPM-inte
43	70	66.7	13	8 ADT79007	Adt79007 Human p53
44	70	66.7	15	8 ADT78987	Adt78987 DNA-PK as
45	69	65.7	15	3 AAB29162	Aab29162 Peptide #

# ALIGNMENTS

RESULT 1  
AAW82321 standard; peptide; 19 AA.

AAW82321;

22-FEB-1999 (first entry)

p53 homologue TIP peptide.

p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medication.

Synthetic.

MO9847919-A1.

29-OCT-1998.

20-APR-1998; 98WC-GB001140.

22-APR-1997; 97GB-00008089.

(UYDU-) UNITV DUNDEE.

Lane DP;

WPI; 1998-609975/51.

New substance with a mdm2 binding domain and coupling partner - useful for stabilising in cells without an efficient mdm2-mediated degradation pathway.

Disclosure; Fig 1; 52pp; English.

This sequence is a peptide homologue of a region of p53 which binds to mdm2. This peptide is used in the construction of a novel agent capable of disrupting the binding of p53 and mdm2 or inhibiting the production of mdm2 in a population of cells. This agent is also used in the preparation of a therapeutic for activating p53, where the population of cells do not overexpress mdm2. Inhibiting mdm2 production and/or inhibiting the binding of mdm2 to p53 allows levels of p53 to increase by reducing the clearance of p53 by mdm2, and can be used to activate p53 function. The agents for use in therapeutics for activating p53 can be used for the treatment of cancer, viral conditions or other conditions associated with non-functional p53

SQ Sequence 19 AA:

Query Match 100.0%; Score 105; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSOETFSDLWKLLPENG 19  
1 PPLSOETFSDLWKLLPENG 19  
DB 1 PPLSOETFSDLWKLLPENG 19

RESULT 2

AAW82319

ID AAW82319 standard; peptide; 19 AA.

AC AAW82319;

DT 22-FEB-1999 (first entry)

XX p53 homologue TIP peptide.

XX p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.

XX Synthetic.

XX WO9847525-A1.

XX 29-OCT-1998.

XX 20-APR-1998; 98WO-GB001144.

XX 22-APR-1997; 97GB-00008092.

XX (UYDU-) UNITV DUNDEE.

XX Lane DP;

XX WPI; 1998-609932/51.

PT New agents which inhibit interaction of p53 and mdm2 - useful for  
activating p53, e.g. for treating cancers; viral conditions or other  
conditions associated with non functional p53 or mdm2.

XX Disclosure; Fig 1; 52pp; English.

CC This sequence is a peptide homologue of a region of p53 which binds to  
CC mdm2. This peptide is used in the construction of a novel agent capable  
CC of disrupting the binding of p53 and mdm2 or inhibiting the production of  
CC mdm2 in a population of cells. This agent is also used in the preparation  
CC of a therapeutic for activating p53, where the population of cells do not  
CC overexpress mdm2. Inhibiting mdm2 production and/or inhibiting the  
CC binding of mdm2 to p53 allows levels of p53 to increase by reducing the  
CC clearance of p53 by mdm2, and can be used to activate p53 function. The  
CC agents for use in therapeutics for activating p53 can be used for the  
CC treatment of cancer, viral conditions or other conditions associated with  
CC non-functional p53

XX Sequence 19 AA:

Query Match 100.0%; Score 105; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSOETFSDLWKLLPENG 19  
1 PPLSOETFSDLWKLLPENG 19  
DB 1 PPLSOETFSDLWKLLPENG 19

RESULT 3

AAW37228

ID AAW37228 standard; peptide; 18 AA.

XX AAW37228;

XX 20-JUL-1998 (first entry)

XX p53 N-terminal peptide fragment for Elisa TIP assay.

DE MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
KM tumour; diagnosis; binding; viral infection; Elisa TIP assay.

XX Homo sapiens.

XX WO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-BP003549.

XX 05-JUL-1996; 96GB-00014197.

XX 07-APR-1997; 97GB-00007041.

XX (NOVS ) NOVARTIS AG.

XX (CANC-) CANCER RES CAMPALGN TECHNOLOGY.

XX Lane D, Boettger V, Boettger A, Picklesley S, Hochkeppel H;

XX Garcia-Echeverria C, Chene P, Furet P;

XX WPI; 1998-100996/09.

PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
PT useful in, e.g. diagnosis and treatment of cancer and viral infections  
PT and identifying binding agents.

PS Disclosure; Page 34; 45pp; English.

CC This represents a p53 N-terminal peptide fragment used in an Elisa TIP  
CC assay for analysing the interaction between human oncogenic protein MDM2  
CC and p53. The invention provides peptide derivatives capable of binding to  
CC the human MDM2. These peptides can specifically inhibit or block the  
CC binding of MDM2 to the human p53 protein, in vitro or in vivo. Inhibiting  
CC the interaction between the p53 and MDM2 can induce growth arrest or  
CC apoptosis in tumour cells comprising a wild-type p53 and non-elevated  
CC levels of MDM2. The peptides may be used to identify molecules that bind  
CC to MDM2 and to identify and design inhibitors of MDM2/p53 binding. They  
CC may also be used to purify binding partners especially MDM2, diagnose  
CC disease by measuring levels of MDM2 in blood of cancer and leukaemia  
CC patients and for treatment or prevention of disease involving p53/MDM2  
CC interactions, especially tumours and viral infections. The peptides can  
CC be administered nasally, rectally, orally or by injection. By interfering  
CC with MDM2/p53 interaction, the peptides can activate p53 function and  
CC accumulation in normal cells. The peptides which mimic the MDM2 binding  
CC site in p53, have a significantly greater blocking activity compared with  
CC wild-type p53

XX Sequence 18 AA:

Query Match 94.3%; Score 99; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSOETFSDLWKLLPEN 18  
1 PPLSOETFSDLWKLLPEN 18  
DB 1 PPLSOETFSDLWKLLPEN 18

RESULT 4

AAW47074

ID AAW47074 standard; peptide; 19 AA.

XX AAW47074;

XX 19-MAY-1998 (first entry)

XX p53/RB interaction inhibiting peptide 6 (residues 11-29 of human p53).

KM Retinoblastoma gene; Rb; p53 protein; interaction; inhibitor; tumour;  
XX apoptosis; modulator; medicine; veterinary; human.  
OS Synthetic.  
OS Homo sapiens.  
XX MO9741433-A1.  
XX PD 06-NOV-1997.  
XX PF 29-APR-1997; 97MO-GB001168.  
XX PR 29-APR-1996; 96GB-00008937.  
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
XX PA Kousarides T;  
XX PI WPI; 1997-549887/50.  
XX DR  
XX PT Identifying compounds that modulate interaction of p53 and Rb protein -  
XX for those that bind to Rb protein, used to induce apoptosis, specifically  
XX PT for treatment of tumors.  
XX PS Claim 36; Page 63; 83pp; English.  
XX CC This peptide fragment of p53 is an inhibitor of the interaction between a  
XX CC p53 protein and a retinoblastoma (Rb) protein. This peptide corresponds  
XX CC to residues 11-29 of human p53 (AAW47079). The interaction between p53  
XX CC and Rb is found to be critical for determining whether or not a cell  
XX CC enters apoptosis. Apoptosis is prevented if interaction occurs. The  
XX CC interaction is between regions 1-71 or 290-393 of p53 and region 379-928  
XX CC of Rb. The invention provides methods to identify compounds able to  
XX CC modulate interaction or binding between p53 and Rb protein. The method  
XX CC comprises combining p53 and Rb, or their fragments, with a test compound  
XX CC and detecting interaction/binding between them. These inhibitory  
XX CC compounds are used in human or veterinary medicine to modulate p53  
XX CC activity and processes, specifically for inducing apoptosis in tumour  
XX CC cells (possibly also in cells infected by virus), in vivo or in vitro.  
XX CC Expression of these modulators by gene therapy methods is also  
XX CC contemplated. Other activities that can be affected are transcription  
XX CC repression, G1 arrest, DNA repair, homologous recombination and 3'-5'-  
XX CC exonuclease activity. Modulation of interaction with Rb may also  
XX CC stabilise p53  
XX CC  
XX SQ Sequence 19 AA;  
XX  
XX Query Match 92.4%; Score 97; DB 2; Length 19;  
XX Best Local Similarity 94.4%; Pred. No. 3.3e-08;  
XX Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 PPLSQETFSDDLWKLPEN 18  
XX 2 PPLSQETFSDDLWKLPEN 19  
XX DB  
XX  
XX RESULT 5  
XX AAE30870  
XX ID AAE30870 standard; peptide; 19 AA.  
XX AC AAE30870;  
XX XX  
XX DT 24-FEB-2003 (first entry)  
XX XX  
XX DE Peptide used in modulating the binding of p53 to p300.  
XX XX  
XX KM p53 polypeptide; p300 polypeptide; cell cycle; cell death; gene therapy;  
XX KM cancer; ischaemia; cytostatic; vasotropic.  
XX XX  
XX OS Unidentified.  
XX OS  
XX PN WO200265134-A2.  
XX XX

PD 22-AUG-2002.  
XX XX  
XX PF 13-FEB-2002; 2002MO-GB000640.  
XX XX  
XX PR 13-FEB-2001; 2001GB-00003508.  
XX XX  
XX PA (UYDU-) UNIV DUNDEE.  
XX XX  
XX PI Hupp TR, Dorman D;  
XX XX  
XX DR WPI; 2003-018623/01.  
XX XX  
XX PT New peptide for modulating the binding of p53 polypeptide to p300  
XX PT polypeptide, useful for regulating the mammalian cell cycle for the  
XX PT treatment of cancer or ischemia.  
XX XX  
XX PS Claim 14; Page 66; 87pp; English.  
XX XX  
XX CC The invention relates to a peptide for use in modulating the binding of a  
XX CC p53 polypeptide to a p300 polypeptide. The new peptide is useful in  
XX CC modulating the binding of a p53 polypeptide to a p300 polypeptide. The  
XX CC peptide may be used to regulate the mammalian cell cycle or to induce or  
XX CC prevent cell death, for the treatment of cancer or ischaemia. The  
XX CC invention is useful in gene therapy. The present sequence is a peptide  
XX CC used in modulating the binding of p53 to p300  
XX CC  
XX SQ Sequence 19 AA;  
XX  
XX Query Match 90.5%; Score 95; DB 6; Length 19;  
XX Best Local Similarity 94.4%; Pred. No. 6.9e-08;  
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX QY 1 PPLSQETFSDDLWKLPEN 18  
XX 2 PPLSQETFSDDLWKLPEN 19  
XX DB  
XX  
XX RESULT 6  
XX ABG73435  
XX ID ABG73435 standard; peptide; 19 AA.  
XX AC ABG73435;  
XX XX  
XX DT 01-MAY-2003 (first entry)  
XX XX  
XX DE Human p53 peptide fragment #4.  
XX XX  
XX KM Human; p53; degradation; cervical cancer; tumour; ovarian cancer; glioma;  
XX KM carcinoma; squamous cell carcinoma; lung cancer; pancreatic cancer;  
XX KM leukemia; lymphoma; neuroblastoma; sarcoma; osteosarcoma; glioblastoma;  
XX KM colon carcinoma; melanoma; choriocarcinoma; breast carcinoma;  
XX KM neuroblastoma; rhabdomyosarcoma; Mdm2; cytostatic; antitumour.  
XX XX  
XX OS Homo sapiens.  
XX XX  
XX PN US2002132977-A1.  
XX XX  
XX PD 19-SEP-2002.  
XX XX  
XX PF 07-DEC-2000; 2000US-00732384.  
XX XX  
XX PR 08-DEC-1999; 99US-0169816P.  
XX XX  
XX PA (YUAN/) YUAN Z.  
XX PA (GUJ/) GU J.  
XX XX  
XX PI Yuan Z, Gu J;  
XX XX  
XX DR WPI; 2003-197937/19.  
XX XX  
XX PT Novel polypeptide that inhibits degradation of endogenous p53 in a  
XX PT mammalian cell, useful for treating cancer, e.g. cervical cancer or a  
XX PT tumor such as sarcoma or carcinoma.

XX Example 5; Page 9; 21pp; English.

XX The invention relates to a substantially pure polypeptide that inhibits

CC degradation of endogenous p53 in a mammalian cell. The polypeptide or a

CC synthetic polypeptide comprising a region of the pure polypeptide is

CC useful for inhibiting degradation of endogenous p53 in a mammalian cell,

CC e.g. in cervical cancer cells or tumour cells selected from sarcoma,

CC carcinoma, squamous cell carcinoma, ovarian cancer, lung cancer,

CC pancreatic cancer, leukaemia, lymphoma, glioma, neuroblastoma,

CC osteosarcoma, colon carcinoma, melanoma, choriocarcinoma, breast

CC carcinoma, glioblastoma, neuroblastoma and rhabdomyosarcoma cells. The

CC cell comprises an Mdm2 amplification or overexpresses Mdm2. A degradation

CC -resistant p53 polypeptide is useful for inhibiting tumour growth, where

CC the tumour is a cervical cancer and comprises a p53 mutation. The

CC polypeptide, and DNA encoding the polypeptide, are useful for treating

CC cancer. This sequence represents a region of the human p53 polypeptide

CC which does not form part of an inhibitory peptide

XX Sequence 19 AA;

XX

XX Query Match 87.6%; Score 92; DB 6; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 2.1e-07;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLSQETFSIDLWKLLPEN 18

DB 1 PLSQETFSIDLWKLLPEN 17

XX

XX RESULT 7

XX ADR20234

XX ID ADR20234 standard; peptide; 19 AA.

XX

XX ADR20234;

XX

XX 04-NOV-2004 (first entry)

XX

XX Mixed element capture agent study associated peptide Gal80bp.

XX

XX target molecule detection; binding element; concomitant binding;

XX medical diagnostic device; research; medicine; military; forensic;

XX diagnostic; biological pathway; protein detection;

XX mixed element capture agent study.

XX

XX Synthetic.

XX

XX US2004161798-A1.

XX

XX 19-AUG-2004.

XX

XX 09-JAN-2004; 2004US-00754457.

XX

XX 09-JAN-2003; 2003US-0438805P.

XX

XX (KODA/) KODADEK T.

XX

XX KODADEK T;

XX

XX MPI; 2004-593073/57.

XX

XX Composition useful for assessing presence of first target molecule such

XX as polypeptide in sample e.g., blood, comprises several low-to-moderate

XX affinity binding elements distributed on surface of, and operatively

XX coupled to support.

XX

XX Example 2; SEQ ID NO 9; 58pp; English.

XX

XX The invention describes a composition (I) for assessing the presence of

XX at least a first target molecule in a sample, comprising: several low-to-

XX moderate affinity binding elements distributed on a surface of, and

XX operatively coupled to a support, where concomitant binding of the first

XX target molecule to two or more of the binding elements results in a high

CC affinity interaction with the first target molecule; or chimeric binding

CC elements distributed on a surface of, and operatively coupled to a

CC support, where concomitant binding of the first target molecule to two or

CC more of the chimeric binding elements results in a high affinity

CC interaction with the first target molecule. (I) is useful for assessing

CC the presence of at least a first target molecule such as polypeptide

CC which is modified in a sample e.g. blood or urine. (I) is useful for

CC determining the presence of a target molecule, which is a modified

CC protein in a sample. The binding elements of (I) are useful: in the

CC construction of medical diagnostic devices; research; medicine; military;

CC forensic; diagnostic application; detecting presence or absence of

CC multiple biological markers in complex samples such as blood or urine;

CC and detecting components of a biological pathway. The binding elements of

CC (I) interact with the target molecule with high affinity and specificity.

CC (I) enables detection of substances from a variety of samples in a rapid

CC high throughput format. The binding elements of (I) are easily produced

CC in large quantities with efficient quality control and can be easily

CC tailored to allow attachment to surfaces. (I) provides an easy,

CC reproducible and cost-effective method of screening, detecting and

CC characterising various components from a variety of samples. The binding

CC elements are suitable for capturing low abundance polypeptides in the

CC sample. The binding elements are suitable in high throughput, robust

CC technology that makes it suitable in military, medical and research

CC field. The binding elements enable sensitive detection of target e.g.,

CC proteins. This is the amino acid sequence of a peptide used in a mixed

CC element capture agent study associated with the composition of the

CC invention.

XX

XX Sequence 19 AA;

XX

XX Query Match 87.6%; Score 92; DB 8; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 2.1e-07;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLSQETFSIDLWKLLPEN 18

DB 1 PLSQETFSIDLWKLLPEN 17

XX

XX RESULT 8

XX AAE30872

XX ID AAE30872 standard; peptide; 16 AA.

XX

XX AAE30872;

XX

XX 24-FEB-2003 (first entry)

XX

XX BOX-1 domain peptide for p300 binding.

XX

XX p53 polypeptide; p300 polypeptide; cell cycle; cell death; gene therapy;

XX cancer; ischaemia; cytostatic; vasotropic.

XX

XX Unidentified.

XX

XX WO200265134-A2.

XX

XX 22-AUG-2002.

XX

XX 13-FEB-2002; 2002WO-GB000640.

XX

XX 13-FEB-2001; 2001GB-00003508.

XX

XX (UYDU-) UNIV DUNDEE.

XX

XX Hupp TR, Dorman D;

XX

XX MPI; 2003-018623/01.

XX

XX New peptide for modulating the binding of p53 polypeptide to p300

XX polypeptide, useful for regulating the mammalian cell cycle for the

XX treatment of cancer or ischemia.

XX

XX Example 2; Fig 6C; 87pp; English.

XX The invention relates to a peptide for use in modulating the binding of a  
CC p53 polypeptide to a p300 polypeptide. The new peptide is useful in  
CC modulating the binding of a p53 polypeptide to a p300 polypeptide. The  
CC peptide may be used to regulate the mammalian cell cycle or to induce or  
CC prevent cell death, for the treatment of cancer or ischemia. The  
CC invention is useful in gene therapy. The present sequence is BOX-1 domain  
CC peptide for p300 binding  
XX  
SQ Sequence 16 AA;  
Query Match 83.8%; Score 88; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.5e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDLWKLLP 16  
1 PPLSQETFSDLWKLLP 16  
Db 1 PPLSQETFSDLWKLLP 16  
RESULT 9  
AEFI6088  
ID AEFI6088 standard; peptide; 16 AA.  
XX  
AC AEFI6088;  
XX  
DT 09-MAR-2006 (first entry)  
XX  
XX Novel stabilized alpha-helix peptide structure-related peptide #5.  
DE  
XX  
KM protein structure; cytosolic; virucide; cell proliferation;  
KM viral replication; gene expression; cell signaling.  
XX  
OS Unidentified.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "N-terminal acetyl"  
FT Modified-site 16 /note= "C-terminal amide"  
XX  
XX US2006008848-A1.  
PN  
PD 12-JAN-2006.  
XX  
XX 09-JUN-2005; 2005US-00148976.  
PF  
XX  
PR 18-MAY-1999; 99US-0134708P.  
PR 26-NOV-1999; 99US-0167634P.  
PR 18-MAY-2000; 2000US-00574086.  
XX  
XX (VERD/) VERDINE G L.  
PA (SCHA/) SCHAFFMEISTER C E.  
XX  
PI Verdine GL, Schaffmeister CE;  
XX  
XX WPI; 2006-088591/09.  
DR  
XX  
XX New stabilized alpha-helix peptide structure useful in medicinal  
PT chemistry as therapeutic agents comprises selected number of any  
PT combination of natural and unnatural amino acids, where the peptide  
PT further comprises cross-linking moieties.  
XX  
XX Disclosure; Fig 16; 34pp; English.  
PS  
XX This invention relates to a novel stabilized alpha-helix peptide  
CC structure which comprises a selected number of any combination of natural  
CC and unnatural amino acids (where the peptide further comprises at least  
CC one cross-linking moiety that stabilizes the peptide in alpha-helix  
CC conformation). The invention may be useful for the development of  
CC compounds with a cytosolic or virucide activity acting as a cell  
CC proliferation inhibitor, viral replication inhibitor, gene expression or

CC other cell signaling process inhibitor. The stabilized alpha-helix  
CC peptide structure generates stabilized-helical structures, as well as  
CC other secondary structures, to enable the investigation of complex  
CC structure-function relationships in proteins and enable the development  
CC of new therapeutic incorporating specific stabilized secondary structure  
CC motifs. The peptides can be synthesized one-at-a-time, using a  
CC traditional peptide to generate the structure motif, and may control  
CC (promote or inhibit) cell functions. The present sequence is that of a  
CC peptide which was used during the exemplification of the novel stabilized  
CC alpha-helix peptide structures of the invention.  
XX  
SQ Sequence 16 AA;  
Query Match 81.0%; Score 85; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 LSOETFSDLWKLLPEN 18  
1 LSOETFSDLWKLLPEN 16  
Db 1 LSOETFSDLWKLLPEN 16  
RESULT 10  
AAV06310  
ID AAV06310 standard; peptide; 15 AA.  
XX  
XX AAV06310;  
XX  
AC AAV06310;  
XX  
DT 06-SEP-1999 (first entry)  
XX  
XX Human p53 peptide (aa13-27).  
DE  
XX  
XX RB18A; p53 regulatory protein; apoptosis; neoplasia; inflammation;  
KM wound healing; graft rejection; reperfusion injury;  
KM myocardial infarction; stroke; traumatic brain injury;  
KM neurodegenerative disease; ischemia; toxemia; infection; AIDS;  
KM hepatitis; breast cancer; ovarian cancer; colon cancer; diagnosis;  
KM therapy; human.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO9931231-A1.  
XX  
XX 24-JUN-1999.  
PD  
XX  
PF 14-DEC-1998; 98WO-EP008560.  
XX  
XX 15-DEC-1997; 97EP-00403051.  
PR  
XX  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
XX  
XX Frade R;  
PI  
XX  
XX WPI; 1999-395177/33.  
DR  
XX  
XX New p53 regulatory protein (RB18A) useful as, e.g. sources of probes and  
PT primers to detect the transcription rate and abundance of RB18A mRNA in  
PT lymphocytes.  
XX  
XX Example 1; Page 25; 87pp; English.  
PS  
XX This synthetic peptide corresponds to amino acids 13-27 of human p53. It  
CC was used to raise anti-peptide p53.1 and anti-RB18A antibodies in rabbit.  
CC RB18A (see AAV06309) is a novel p53 regulatory protein of the invention.  
CC The antibodies were used in immunoscreenings that led to the isolation of  
CC a cDNA clone (see AAX59124) encoding human RB18A. The invention provides  
CC methods and compositions for the diagnostic and therapeutic applications  
CC of RB18A, in particular for the diagnosis, prevention or treatment of  
CC neoplasia  
XX  
SQ Sequence 15 AA;  
Query Match 77.1%; Score 81; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 9.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLP 16  
| | | | | | | | | | | | | | | |  
Db 1 PLSQETFSDLWKLLP 15

RESULT 11  
ABG75806  
ID ABG75806 standard; peptide; 15 AA.  
XX  
XX ABG75806;  
AC  
XX  
DT 08-MAY-2003 (first entry)  
XX  
DE Solid phase precipitation and extraction method peptidyl-resin #1.  
XX  
KW SPPE; solid phase precipitation and extraction; analyte;  
KW solid-phase extraction; SPB; peptide synthesis; chromatography;  
KW light scattering detector; ether; trifluoroacetic acid; peptidyl-resin.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER= modified with Bu (not defined in the  
FT specification)"  
FT Modified-site 2 /label= OTHER  
FT /note= "OTHER= modified with Trt (not defined in the  
FT specification)"  
FT Modified-site 3. .4 /label= OTHER  
FT /note= "OTHER= modified with Bu (not defined in the  
FT specification)"  
FT Modified-site 5. .7 /label= OTHER  
FT /note= "OTHER= modified with Bu (not defined in the  
FT specification)"  
FT Modified-site 9. .10 /label= OTHER  
FT /note= "OTHER= modified with t-butylloxycarbonyl (Boc)"  
FT Modified-site 14 /label= OTHER  
FT /note= "OTHER= modified with Bu (not defined in the  
FT specification)"  
FT Modified-site 15 /label= OTHER  
FT /note= "OTHER= modified with Trt (not defined in the  
FT specification) and linked to the Tentagel resin"  
XX  
XX US6479296-B1.  
XX  
XX 12-NOV-2002.  
XX  
XX 06-JUL-2000; 2000US-00610761.  
XX  
XX 07-JUL-1999; 99US-0142582P.  
XX  
XX (BONN/) BONNER A. G.  
XX (UDELL/) UDELL L. S.  
XX (CREA/) CREASEY W. A.  
XX (DULY/) DULY S.  
XX (LAUR/) LAURSEN R. A.  
XX  
XX Bonner AG, UdeLL LS, Creasey WA, Duly S, Laursen RA;  
XX  
XX WPI; 2003-298114/29.  
XX  
XX Isolation of biological analyte, e.g. protein, from sample, e.g. aqueous  
XX and/or organic solvent, involves precipitating biological analyte on  
PT

PT solid-phase extraction device, and eluting precipitated analyte from  
PT extraction device.  
XX  
XX Example; Col 4; 16pp; English.  
XX  
XX The invention discloses a method for the isolation of a biological  
XX analyte (e.g. a protein and/or nucleic acid from a sample or aqueous  
XX and/or organic solvent) which comprises the precipitation of the  
XX biological analyte on a solid-phase extraction (SPE) media or device  
XX followed by elution of the precipitated biological analyte off the  
XX extraction media or device. The method is referred to as the solid phase  
XX precipitation and extraction (SPPE) method. The method can be used in  
XX peptide synthesis chemistry and in the purification of combinatorially-  
XX derived compound libraries which are the basis for drug delivery efforts  
XX in pharmaceutical companies. It is also useful in sample preparation and  
XX analytical, preparative and process chromatography with monitoring by an  
XX evaporative light scattering detector. The method overcomes the  
XX disadvantages of the ether precipitation method, such as handling of  
XX flammable ether and corrosive trifluoroacetic acid solutions, and the  
XX handling and manipulation of milligram amounts of precipitate. The method  
XX can be automated without difficulty and provides convenience for multiple  
XX sample handling. The sequence presented is an example of a SPPE peptidyl-  
XX resin  
XX  
SQ Sequence 15 AA;  
XX  
XX Query Match 77.1%; Score 81; DB 6; Length 15;  
XX Best Local Similarity 100.0%; Pred. No. 9.3e-06;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SOETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | |  
Db 1 SOETFSDLWKLLPEN 15

RESULT 12  
ADC22292  
ID ADC22292 standard; peptide; 15 AA.  
XX  
XX ADC22292;  
AC  
XX 18-DEC-2003 (first entry)  
XX  
XX Protein binding domain amino acid sequence SEQ ID NO:141.  
XX  
XX DE  
XX recombinant fusion protein; fusion protein; binding; detection;  
XX KW localisation domain; binding domain;  
XX KW subcellular compartment localisation.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX PN MO2003012068-A2.  
XX  
XX 13-FEB-2003.  
XX  
XX PD 01-AUG-2002; 2002WO-US024572.  
XX  
XX PF 01-AUG-2001; 2001US-0309395P.  
XX  
XX PR 13-DEC-2001; 2001US-0341589P.  
XX  
XX (CELL-) CELLOMICS INC.  
XX  
XX PA  
XX PI Bright G, Premkumar DR, Chen Y;  
XX  
XX WPI; 2003-248174/24.  
XX  
XX DR N-PSDB; ADC22293.  
XX  
XX  
XX New recombinant fusion protein comprising detection and first  
XX localization domains and a binding domain for the molecule of interest,  
XX useful for detecting binding of a molecule of interest.  
XX  
XX Claim 8; SEQ ID NO 141; 101pp; English.  
XX

CC The present invention describes a recombinant fusion protein (I) for  
CC detecting binding of a molecule of interest. (I) comprises: (a) a  
CC detection domain; (b) a first localisation domain; and (c) a binding  
CC domain for the molecule of interest. The detection domain, the first  
CC localisation domain and the binding domain for the molecule of interest  
CC constituting the recombinant fusion protein for detecting binding of a  
CC molecule of interest are operably linked. The binding domain for the  
CC molecule of interest is separated from the first localisation domain by 0  
CC -20 amino acid residues. The first localisation domain and the binding  
CC domain for the molecule of interest both do not occur in a single non-  
CC recombinant protein with the same spacing as in the recombinant fusion  
CC protein for detecting binding of a molecule of interest. Also described:  
CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;  
CC (2) a recombinant expression vector comprising the nucleic acid control;  
CC sequences operably linked to the recombinant nucleic acid molecule; (3) a  
CC genetically engineered host cell transfected with the recombinant  
CC expression vector; (4) a kit for detecting binding of the molecule of  
CC interest; and (5) a method for identifying compounds that alter the  
CC binding of the molecule of interest. The recombinant fusion protein is  
CC useful for detecting binding of a molecule of interest. The recombinant  
CC fusion protein eliminates the need to construct two or more chimeric  
CC proteins and enables the monitoring of biochemical events in live, intact  
CC or fixed cells. The present sequence is used in the exemplification of  
CC the present invention.

CC  
XX  
SQ Sequence 15 AA;

Query Match 77.1%; Score 81; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSFLMKLL 15  
|||  
Db 1 PPLSQETFSFLMKLL 15

RESULT 13

ID ADG78883 standard; peptide; 15 AA.

XX ADG78883;

DT 11-MAR-2004 (first entry)

DE Human p53 protein peptide PNC27 (residues 12-26).

XX Human; p53; cytosolic.

XX Homo sapiens.

XX WO2003105880-A1.

PD 24-DEC-2003.

PF 12-MAR-2003; 2003WO-US007687.

PR 12-MAR-2002; 2002US-0363785P.

PA (UANY ) UNIV NEW YORK STATE RES FOUND.

XX (PINC/) PINCUS M R.

DR WPI; 2004-090756/09.

PT New peptides useful for treatment of neoplastic diseases comprises amino  
acid sequence of cell cycle regulatory protein.

PS Claim 2; SEQ ID NO 1; 32pp; English.

XX The present sequence is that of a peptide (PNC27) comprising amino acid  
residues 12-26 of human p53. The invention provides peptides  
corresponding to all or a portion ADG78884-ADG78885 of this sequence, the  
peptides being lethal to malignant or transformed cells when fused to a  
membrane-penetrating leader sequence. The peptides are thus useful for

CC treating neoplastic disease in an animal, preferably a human. Claimed  
CC methods of selectively killing malignant or neoplastic cells comprise  
CC administering the p53-derived peptide fused at its C-terminus to a  
CC membrane-penetrating leader sequence, such as the penetratin leader  
CC sequence ADG78886.

CC  
XX  
SQ Sequence 15 AA;

Query Match 77.1%; Score 81; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSFLMKLL 15  
|||  
Db 1 PPLSQETFSFLMKLL 15

RESULT 14

ID ADN48957 standard; peptide; 15 AA.

XX ADN48957;

DT 01-JUL-2004 (first entry)

DE Peptide #1 from human p53 protein.

XX Lethal peptide; malignant cell; transformed cell; mammalian;

KW membrane-penetrating leader sequence; human; p53; cell death;

XX neoplastic cell; cytosolic.

XX Homo sapiens.

XX US2004038902-A1.

PD 26-FEB-2004.

PF 12-MAR-2003; 2003US-00386737.

PR 05-APR-2000; 2000US-0195102P.

PR 05-APR-2001; 2001US-00827683.

PR 12-MAR-2002; 2002US-0363785P.

PA (PINC/) PINCUS M R.

XX Pincus MR;

XX WPI; 2004-203289/19.

PT New peptide fused to membrane-penetrating leader sequence and is  
selectively lethal to malignant or transformed cells, useful for treating  
neoplastic or malignant cells, e.g. cancer cells.

PS Claim 2; SEQ ID NO 1; 9pp; English.

XX The present invention relates to peptides that are selectively lethal to  
CC malignant and transformed mammalian cells when fused to a membrane-  
CC penetrating leader sequence. The peptides are derived from the human p53  
CC protein. Also disclosed are (i) a pharmaceutical composition comprising  
CC at least one of the peptides or its analogues or derivatives admixed with  
CC a pharmaceutical carrier, and (ii) a method of selectively killing  
CC malignant or neoplastic cells in a subject. The leader sequence is  
CC preferably located at the carboxy terminal end of the peptide, its  
CC analogue or derivative. The leader sequence comprises predominantly  
CC positively charged amino acid residues. The leader sequence is at least  
CC one of penetratin, Arg98, Tat of HIV1, D-TAT, R-TAT, SV40-NLS,  
CC nucleoplasmin-NLS, HIV REV, FHV coat, BMV GAG, HTLV-II (REX),  
CC P22N, Lambda N, Delta N, yeast Prpe, human D2AF, human C-FOS, human C-  
CC JUN, yeast GCN4 or P-vec. Selectively killing malignant or neoplastic  
CC cells in a subject comprises administering to the subject an amount of  
CC the peptide, where a membrane-penetrating leader sequence is fused to the  
CC carboxy terminal of the peptide, its analogue or derivative. The present  
CC sequence represents a peptide of the invention.

XX SQ Sequence 15 AA;

Query Match 77.1%; Score 81; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSOETFSDLWKLL 15  
 |||||  
 DB 1 PPLSOETFSDLWKLL 15

RESULT 15  
 ADQ90921  
 ID ADQ90921 standard; peptide; 15 AA.  
 AC ADQ90921;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE Pancreatic cancer associated antigen related peptide SEQ ID NO:1.  
 XX  
 KW pancreatic carcinoma-specific antigen 3C4-Ag; pancreatic cancer;  
 XX antibody; cytostatic; immunotoxin; pancreatic cancer associated antigen.  
 OS Synthetic.  
 MO2004065547-A2.  
 PN  
 PD 05-AUG-2004.  
 XX  
 PF 16-JAN-2004; 2004WO-US001196.  
 XX  
 PR 17-JAN-2003; 2003US-0440699P.  
 XX  
 (UYNV ) UNITV NEW YORK STATE RES FOUND.  
 PA  
 PI Michl J, Bradu SM, Hannan R, Pincus MR;  
 XX  
 DR WPI; 2004-571676/55.  
 XX  
 PT New pancreatic carcinoma-specific antigen 3C4-Ag primarily localized on  
 PT the surface of rat and human pancreatic cancer cells, but not detected in  
 PT normal, non-proliferating cells, useful in diagnosis and treatment of  
 PT pancreatic cancer.  
 XX  
 PS Claim 15; SEQ ID NO 1; 112pp; English.  
 XX  
 CC The present invention describes the pancreatic carcinoma-specific antigen  
 CC 3C4-Ag in substantially purified form, which has a molecular weight of  
 CC 43.5 kDa as determined by SDS-PAGE, and a pI on isoelectrofocusing of 4.5  
 CC -5.0. The antigen is unglycosylated or minimally glycosylated and is  
 CC primarily localised on the surface of rat and human pancreatic cancer  
 CC cells but is not detected in normal, non-proliferating cells. Also  
 CC described: (1) a soluble pancreatic carcinoma-specific antigen 3C4-Ag  
 CC having a molecular weight of 36-38 kDa as determined by SDS-PAGE which is  
 CC isolatable from sera and other bodily fluids of pancreatic cancer  
 CC patients; (2) an immunologically active fragment of the pancreatic  
 CC carcinoma-specific antigen 3C4-Ag; (3) an antibody or its binding portion  
 CC having specificity to pancreatic carcinoma specific antigen 3C4-Ag; (4) a  
 CC murine hybridoma cell line that produces a monoclonal antibody  
 CC specifically immunoreactive with the 3C4-Ag antigen; (5) a monoclonal  
 CC antibody, mb3c4, secreted by the hybridoma cell line; (6) detecting  
 CC pancreatic cancer in an animal subject, comprising: (a) contacting a  
 CC cell, tissue, or fluid sample from the subject with (the binding portion  
 CC of) an antibody that binds to 3C4-Ag; (b) detecting antibody-antigen  
 CC complex in the sample; and (c) correlating the detection of elevated  
 CC levels of antibody-antigen complex in the sample with the presence of  
 CC pancreatic cancer; (7) a diagnostic kit for detecting 3C4-Ag in a cell,  
 CC tissue or fluid sample from a patient comprising: (a) the antibody or its  
 CC binding portion specific for 3C4-Ag or its immunologically active  
 CC fragment; (b) a conjugate of a specific binding partner for the antibody  
 CC or its binding portion; and (c) a label for detecting the bound antibody;

CC (8) treating pancreatic cancer in a patient by administering an effective  
 CC amount of an antibody or its binding portion which specifically binds to  
 CC 3C4-Ag or its immunologically active fragment, where the antibody or  
 CC binding portion is conjugated or linked to a therapeutic drug or toxin;  
 CC and (9) a pharmaceutical composition comprising the antibody or its  
 CC binding portion, and a carrier. The pancreatic carcinoma-specific antigen  
 CC 3C4-Ag has cytostatic activity, and can be used as an immunotoxin. The  
 CC antigen and methods are useful for detecting and treating pancreatic  
 CC cancer. The present sequence represents a pancreatic cancer associated  
 CC antigen peptide, which is used in the exemplification of the present  
 CC invention.  
 XX

SQ Sequence 15 AA;

Query Match 77.1%; Score 81; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSOETFSDLWKLL 15  
 |||||  
 DB 1 PPLSOETFSDLWKLL 15

Search completed: July 5, 2006, 22:54:22  
 Job time : 194 secs

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OM protein - protein search, using sw model

Run on: July 5, 2006, 23:00:16 ; Search time 181 Seconds  
(without alignments)  
48.625 Million cell updates/sec

Title: US-09-403-440A-2  
Perfect score: 105  
Sequence: 1 PPLSQETFSDFDKLKPENG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 442174

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	94.3	18	3	US-09-214-371-74
2	99	94.3	18	5	US-10-927-262A-74
3	92	87.6	19	3	US-09-732-384-7
4	92	87.6	19	4	US-10-754-457-9
5	92	87.6	19	4	US-10-927-262A-1
6	90	85.7	19	4	US-10-155-059-13
7	89	84.8	19	3	US-09-214-371-1
8	88	83.8	16	4	US-10-467-758-14
9	81	77.1	15	4	US-10-211-088-141
10	81	77.1	15	4	US-10-425-970-4
11	81	77.1	15	6	US-11-019-894A-1
12	81	77.1	17	6	US-11-128-722-14
13	77	73.3	15	3	US-09-732-384-6
14	77	73.3	15	6	US-11-051-411-1109
15	77	73.3	15	6	US-11-051-411-1169
16	75.5	71.9	19	4	US-10-328-953-14
17	74	70.5	16	4	US-10-155-059-23
18	73	69.5	13	5	US-10-948-707-1379
19	73	69.5	14	4	US-10-275-427A-13
20	66	62.9	12	3	US-09-214-371-17
21	66	62.9	12	4	US-10-609-217-131
22	66	62.9	12	4	US-10-609-217-143
23	66	62.9	12	4	US-10-632-388-131
24	66	62.9	12	4	US-10-632-388-143
25	66	62.9	12	4	US-10-651-723-131
26	66	62.9	12	4	US-10-651-723-143
27	66	62.9	12	4	US-10-645-761-131

## ALIGNMENTS

28	66	62.9	12	4	US-10-645-761-143	Sequence 143, App
29	66	62.9	12	4	US-10-666-696-131	Sequence 131, App
30	66	62.9	12	4	US-10-666-696-143	Sequence 143, App
31	66	62.9	12	4	US-10-653-048-131	Sequence 131, App
32	66	62.9	12	4	US-10-653-048-143	Sequence 143, App
33	66	62.9	12	5	US-10-645-784-131	Sequence 131, App
34	66	62.9	12	5	US-10-645-784-143	Sequence 143, App
35	66	62.9	12	5	US-10-927-262A-17	Sequence 17, App
36	66	62.9	12	5	US-10-927-262A-24	Sequence 24, App
37	66	62.9	15	4	US-10-339-712-38	Sequence 38, App
38	66	62.9	15	4	US-10-340-179-18	Sequence 18, App
39	66	62.9	15	5	US-10-927-262A-39	Sequence 39, App
40	65	61.9	15	3	US-09-258-981-3	Sequence 3, App
41	65	61.9	15	3	US-09-550-692-6	Sequence 6, App
42	65	61.9	15	3	US-09-952-680A-55	Sequence 55, App
43	65	61.9	15	5	US-10-215-982-55	Sequence 55, App
44	65	61.9	15	5	US-10-793-943-3	Sequence 3, App
45	65	61.9	15	5	US-10-862-195-2239	Sequence 2239, App

```
RESULT 1
US-09-214-371-74
; Sequence 74, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Botterger, Volker
; APPLICANT: Botterger, Angelica
; APPLICANT: Pickelsley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the interaction of p53 and MDM2
; FILE REFERENCE: 4-20937/A/PT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-74

Query Match          94.3%; Score 99; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PPLSQETFSDFDKLKPEN 18
Db      1 PPLSQETFSDFDKLKPEN 18

RESULT 2
US-10-927-262A-74
; Sequence 74, Application US/10927262A
; Publication No. US20050137137A1
; GENERAL INFORMATION:
; APPLICANT: LANE, DAVID P
; APPLICANT: BOTTERGER, VOLKER
; APPLICANT: BOTTERGER, ANGELICA
; APPLICANT: PICKELSLEY, STEVEN M.
; APPLICANT: HOCHKEPPEL, HEINZ-KURT
; APPLICANT: GARCIA-ECHEVERRIA, CARLOS
; APPLICANT: CHENE, PATRICK
```

```

; APPLICANT: FURET, PASCAL
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
; FILE REFERENCE: 39749.0002 APC CON
; CURRENT APPLICATION NUMBER: US/10/927,262A
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: 2004-08-25
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: GB 9614197.3
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: GB 9707041.1
; PRIOR FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-927-262A-74
```

```

Query Match          94.3%; Score 99; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

Qy      1 PLSQETFSDLWKLLPEN 18
        |||||
Db      1 PLSQETFSDLWKLLPEN 18
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```

RESULT 3
US-09-732-384-7
; Sequence 7, Application US/09732384
; Patent No. US20020132977A1
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; APPLICANT: Gu, Jitae
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein
US-09-732-384-7
```

```

Query Match          87.6%; Score 92; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      2 PLSQETFSDLWKLLPEN 18
        |||||
Db      1 PLSQETFSDLWKLLPEN 17
```

```

RESULT 4
US-10-754-457-9
; Sequence 9, Application US/10754457
; Publication No. US20040161798A1
; GENERAL INFORMATION:
; APPLICANT: KODADER, THOMAS
; TITLE OF INVENTION: METHODS AND COMPOSITIONS COMPRISING CAPTURE AGENTS
```

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; FILE REFERENCE: U7SD:935US
; CURRENT APPLICATION NUMBER: US/10/754,457
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-754-457-9
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```

Query Match          87.6%; Score 92; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      2 PLSQETFSDLWKLLPEN 18
        |||||
Db      1 PLSQETFSDLWKLLPEN 17
```

```

RESULT 5
US-10-927-262A-1
; Sequence 1, Application US/10927262A
; Publication No. US20050-37137A1
; GENERAL INFORMATION:
; APPLICANT: LANE, DAVID P
; APPLICANT: BOTTFGER, VOLKER
; APPLICANT: BOTTFGER, ANGELIKA
; APPLICANT: PICKSLEY, STEVEN M.
; APPLICANT: HOCHKEPPEL, HEINZ-KURT
; APPLICANT: GARCIA-ECHEVERRIA, CARLOS
; APPLICANT: CHENE, PATRICK
; APPLICANT: FURET, PASCAL
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
; FILE REFERENCE: 39749.0002 APC CON
; CURRENT APPLICATION NUMBER: US/10/927,262A
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: 09/214,371
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: GB 9614197.3
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: GB 9707041.1
; PRIOR FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-927-262A-1
```

```

Query Match          87.6%; Score 92; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

Qy      2 PLSQETFSDLWKLLPEN 18
        |||||
Db      1 PLSQETFSDLWKLLPEN 17
```

```

RESULT 6
US-10-155-059-13
; Sequence 13, Application US/10155059
; Publication No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
```

```

; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
;
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-10-155-059-13
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
;
;
; Query Match      85.7%; Score 90; DB 4; Length 19;
; Best Local Similarity 88.9%; Pred. No. 2.3e-06;
; Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY      1 PPLSQETFSDLWKLLPEN 18
; DB      1 PPLSQETFSDLWKLLPEN 18
;
; RESULT 7
; US-09-214-371-1
; Sequence 1, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Botzger, Volker
; APPLICANT: Botzger, Angelica
; APPLICANT: Pickelsley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Fureit, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 19
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```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; US-09-214-371-1
;
; Query Match      84.8%; Score 89; DB 3; Length 19;
; Best Local Similarity 94.1%; Pred. No. 3.3e-06;
; Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY      2 PLSQETFSDLWKLLPEN 18
; DB      1 PLSQETFSDLWKLLPEN 17
;
; RESULT 8
; US-10-467-758-14
; Sequence 14, Application US/10467758
; Publication No. US20040132108A1
; GENERAL INFORMATION:
; APPLICANT: Hupp, Theodore
; APPLICANT: Dornan, David
; TITLE OF INVENTION: Screening Method and Agents
; FILE REFERENCE: 9013.54
; CURRENT APPLICATION NUMBER: US/10/467,758
; CURRENT FILING DATE: 2003-08-13
; PRIOR APPLICATION NUMBER: PCT/GB02/00640
; PRIOR FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: GB 0103508.8
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-467-758-14
;
; Query Match      83.8%; Score 88; DB 4; Length 16;
; Best Local Similarity 100.0%; Pred. No. 3.9e-06;
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY      1 PPLSQETFSDLWKLLP 16
; DB      1 PPLSQETFSDLWKLLP 16
;
; RESULT 9
; US-10-211-088-141
; Sequence 141, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1e1 Fusion Proteins And Assays For Molecular B
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 141
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
; US-10-211-088-141
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Query Match 77.1%; Score 81; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSQETFSDLWKLL 15  
| | | | | | | | | | | | | | |  
DB 1 PLSQETFSDLWKLL 15

RESULT 10  
US-10-425-970-4  
; Sequence 4, Application US/10425970  
; Publication No. US20040052794A1  
; GENERAL INFORMATION:

APPLICANT: PRAD, Raymond  
TITLE OF INVENTION: P53 REGULATORY PROTEIN CALLED RB18A AND USES THEREOF  
FILE REFERENCE: P067810S00/BAS  
CURRENT APPLICATION NUMBER: US/10/425,970  
CURRENT FILING DATE: 2003-04-30  
PRIOR APPLICATION NUMBER: 09/581,472  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: PCT/EP98/08560  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: EP 97403051.2  
PRIOR FILING DATE: 1997-12-15  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: The artificial sequence is a nucleic acid.  
US-10-425-970-4

Query Match 77.1%; Score 81; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLLP 16  
| | | | | | | | | | | | | | | |  
DB 1 PLSQETFSDLWKLLP 15

RESULT 11  
US-11-019-894A-1  
; Sequence 1, Application US/11019894A  
; Publication No. US20050245451A1  
; GENERAL INFORMATION:

APPLICANT: Pincus, Matthew R.  
TITLE OF INVENTION: PEPTIDES SELECTIVELY LETHAL TO THE MALIGNANT AND TRANSFORMED  
FILE REFERENCE: 1181-17 CIP A  
CURRENT APPLICATION NUMBER: US/11/019,894A  
CURRENT FILING DATE: 2004-12-21  
PRIOR APPLICATION NUMBER: 10/386,737  
PRIOR FILING DATE: 2003-03-12  
PRIOR APPLICATION NUMBER: 09/827,683  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/195,102  
PRIOR FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: 60/363,785  
PRIOR FILING DATE: 2002-03-12  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: peptide; amino acid residues 12-26 of human p53 protein  
US-11-019-894A-1

Query Match 77.1%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSQETFSDLWKLL 15  
| | | | | | | | | | | | | | |  
DB 1 PLSQETFSDLWKLL 15

RESULT 12  
US-11-128-722-14  
; Sequence 14, Application US/11128722  
; Publication No. US20060014675A1  
; GENERAL INFORMATION:

APPLICANT: Ayora, Paranjit  
APPLICANT: Chapman, Ross  
TITLE OF INVENTION: METHODS FOR PREPARING INTERNALLY CONSTRAINED PEPTIDES  
FILE REFERENCE: 57953/1281  
CURRENT APPLICATION NUMBER: US/11/128,722  
CURRENT FILING DATE: 2005-05-13  
PRIOR APPLICATION NUMBER: 60/574,964  
PRIOR FILING DATE: 2004-05-27  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 14  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-11-128-722-14

Query Match 77.1%; Score 81; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SOETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | |  
DB 1 SOETFSDLWKLLPEN 15

RESULT 13  
US-09-732-384-6  
; Sequence 6, Application US/09732384  
; Patent No. US20020132977A1  
; GENERAL INFORMATION:

APPLICANT: Yuan, Zhi-Min  
APPLICANT: Gu, Jijie  
TITLE OF INVENTION: Inhibition of p53 Degradation  
FILE REFERENCE: 21508-044  
CURRENT APPLICATION NUMBER: US/09/732,384  
CURRENT FILING DATE: 2000-12-07  
PRIOR APPLICATION NUMBER: 60/169,816  
PRIOR FILING DATE: 1999-12-08  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Protein  
OTHER INFORMATION: fragment not in inhibitory p53 polypeptide  
US-09-732-384-6

Query Match 73.3%; Score 77; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00016;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | |

Db 1 QETFSDLWKLLEN 14

## RESULT 14

US-11-051-411-1109

Sequence 1109, Application US/11051411

Publication No. US20050196403A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Celis, Esteban

APPLICANT: Keogh, Elisea

TITLE OF INVENTION: Inducing Cellular Immune Responses To

FILE REFERENCE: 2060.0120000

CURRENT APPLICATION NUMBER: US/11/051,411

PRIOR FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US/09/458,297

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US 09/017,735

PRIOR FILING DATE: 1998-02-03

PRIOR APPLICATION NUMBER: PCT/US99/13789

PRIOR FILING DATE: 1999-06-17

PRIOR APPLICATION NUMBER: US 09/098,584

PRIOR FILING DATE: 1998-06-17

NUMBER OF SEQ ID NOS: 1492

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1109

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Peptide

US-11-051-411-1109

Query Match 73.3%; Score 77; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00016;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKL 14

Db 2 PPLSQETFSDLWKL 15

## RESULT 15

US-11-051-411-1469

Sequence 1469, Application US/11051411

Publication No. US20050196403A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Celis, Esteban

APPLICANT: Keogh, Elisea

TITLE OF INVENTION: Inducing Cellular Immune Responses To

FILE REFERENCE: 2060.0120000

CURRENT APPLICATION NUMBER: US/11/051,411

PRIOR FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US/09/458,297

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US 09/017,735

PRIOR FILING DATE: 1998-02-03

PRIOR APPLICATION NUMBER: PCT/US99/13789

PRIOR FILING DATE: 1999-06-17

PRIOR APPLICATION NUMBER: US 09/098,584

PRIOR FILING DATE: 1998-06-17

NUMBER OF SEQ ID NOS: 1492

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1469

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Peptide

US-11-051-411-1469

Query Match 73.3%; Score 77; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00016;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKL 14

Db 2 PPLSQETFSDLWKL 15

Search completed: July 5, 2006, 23:04:06  
Job time: 182 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 5, 2006, 23:01:11 ; Search time 21 Seconds  
(Without alignments)  
24.277 Million cell updates/sec

Title: US-09-403-440A-2  
Perfect score: 105  
Sequence: 1 PPLSQETFSDDLWKLPENG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues  
Total number of hits satisfying chosen parameters: 23430

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /EMC\_Celerra\_SIDS3/ProdData/1/pubppaa/US09\_NEW\_PUB pep.\*  
2: /EMC\_Celerra\_SIDS3/ProdData/1/pubppaa/US06\_NEW\_PUB pep.\*  
3: /EMC\_Celerra\_SIDS3/ProdData/1/pubppaa/US07\_NEW\_PUB pep.\*  
4: /EMC\_Celerra\_SIDS3/ProdData/1/pubppaa/US08\_NEW\_PUB pep.\*  
5: /EMC\_Celerra\_SIDS3/ProdData/1/pubppaa/US09\_NEW\_PUB pep.\*  
6: /EMC\_Celerra\_SIDS3/ProdData/1/pubppaa/US10\_NEW\_PUB pep.\*  
7: /EMC\_Celerra\_SIDS3/ProdData/1/pubppaa/US11\_NEW\_PUB pep.\*  
8: /EMC\_Celerra\_SIDS3/ProdData/1/pubppaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	62.9	12	6	US-10-953-613C-778 Sequence 778, App
2	66	62.9	12	6	US-10-953-613C-780 Sequence 790, App
3	61	58.1	12	6	US-10-953-613C-780 Sequence 780, App
4	61	58.1	12	6	US-10-953-613C-792 Sequence 792, App
5	60	57.1	12	6	US-10-953-613C-779 Sequence 779, App
6	57.1	56.2	12	6	US-10-953-613C-791 Sequence 791, App
7	55	52.4	10	6	US-10-538-066-624 Sequence 624, App
8	55	52.4	10	6	US-10-538-066-600 Sequence 600, App
9	55	52.4	12	6	US-10-953-613C-781 Sequence 781, App
10	55	52.4	12	6	US-10-953-613C-793 Sequence 793, App
11	49	46.7	9	6	US-10-538-066-353 Sequence 353, App
12	43	41.0	10	6	US-10-538-066-623 Sequence 623, App
13	42	40.0	9	6	US-10-538-066-354 Sequence 354, App
14	37	35.2	9	6	US-10-538-066-622 Sequence 622, App
15	36	34.3	6	6	US-10-953-613C-777 Sequence 777, App
16	35	33.3	7	6	US-10-538-066-638 Sequence 638, App
17	32	30.5	12	6	US-10-953-613C-583 Sequence 583, App
18	32	30.5	14	7	US-11-118-524-5 Sequence 5, App1
19	31	29.5	12	6	US-10-953-613C-586 Sequence 586, App
20	30	28.6	17	6	US-10-953-613C-894 Sequence 894, App
21	28	26.7	12	6	US-10-953-613C-585 Sequence 585, App
22	27	25.7	10	7	US-11-196-917A-85 Sequence 85, App1
23	27	25.7	12	6	US-10-953-613C-587 Sequence 587, App
24	27	25.7	12	6	US-10-953-613C-590 Sequence 590, App
25	27	25.7	13	7	US-11-313-356-15 Sequence 15, App1

26	27	25.7	15	6	US-10-953-613C-786 Sequence 786, App
27	27	25.7	17	6	US-10-953-613C-907 Sequence 907, App
28	26	24.8	10	7	US-11-219-563-29 Sequence 29, App1
29	26	24.8	10	7	US-11-196-917A-77 Sequence 77, App1
30	26	24.8	11	6	US-10-538-066-4 Sequence 4, App1
31	26	24.8	11	6	US-10-953-613C-595 Sequence 595, App
32	26	24.8	12	6	US-10-953-613C-582 Sequence 582, App
33	26	24.8	12	6	US-10-953-613C-586 Sequence 586, App
34	26	24.8	12	6	US-10-953-613C-557 Sequence 597, App
35	26	24.8	12	6	US-10-953-613C-558 Sequence 598, App
36	26	24.8	19	7	US-11-234-731-561 Sequence 561, App
37	25	23.8	11	7	US-11-134-871-3124 Sequence 3124, App
38	25	23.8	12	6	US-10-953-613C-588 Sequence 588, App
39	25	23.8	17	6	US-10-953-613C-901 Sequence 901, App
40	25	23.8	18	7	US-11-134-871-173 Sequence 173, App
41	25	23.8	18	7	US-11-134-871-3598 Sequence 3598, App
42	25	23.8	19	7	US-11-234-731-292 Sequence 292, App
43	25	23.8	18	7	US-11-134-871-776 Sequence 776, App
44	24	22.9	10	6	US-10-953-613C-789 Sequence 789, App
45	24	22.9	10	7	US-11-301-554-2112 Sequence 2112, App

## ALIGNMENTS

RESULT 1  
US-10-953-613C-778  
Sequence 778, Application US/10953613C  
Publication No. US20060127404A1  
GENERAL INFORMATION:  
APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Chirayeb, John;Seallon;  
APPLICANT: Bernard,Nespor; Thomas  
TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES  
FILE REFERENCE: CEN5038 NP  
CURRENT APPLICATION NUMBER: US/10/953,613C  
CURRENT FILING DATE: 2004-09-29  
PRIOR APPLICATION NUMBER: 60/507,231  
PRIOR FILING DATE: 2003-09-30  
NUMBER OF SEQ ID NOS: 1021  
SOFTWARE: PatentIn Ver 3.0  
SEQ ID NO 778  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-953-613C-778

Query Match 62.9%; Score 66; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00056;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 QETFSDDLWKLP 16  
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Db 1 QETFSDDLWKLP 12  
RESULT 2  
US-10-953-613C-790  
Sequence 790, Application US/10953613C  
Publication No. US20060127404A1  
GENERAL INFORMATION:  
APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Chirayeb, John;Seallon;  
APPLICANT: Bernard,Nespor; Thomas  
TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES  
FILE REFERENCE: CEN5038 NP  
CURRENT APPLICATION NUMBER: US/10/953,613C  
CURRENT FILING DATE: 2004-09-29  
PRIOR APPLICATION NUMBER: 60/507,231  
PRIOR FILING DATE: 2003-09-30  
NUMBER OF SEQ ID NOS: 1021  
SOFTWARE: PatentIn Ver 3.0  
SEQ ID NO 790  
LENGTH: 12  
TYPE: PRT

ORGANISM: Homo sapiens  
US-10-953-613C-790

Query Match 62.9%; Score 66; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00056;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDLWKLLP 16  
| | | | | | | | | | | | | |  
Db 1 QETFSDLWKLLP 12

RESULT 3  
US-10-953-613C-780

Sequence 780, Application US/10953613C  
Publication No. US20060127404A1

GENERAL INFORMATION:

APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallan;  
APPLICANT: Bernard;Nesspor; Thomas

TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES

FILE REFERENCE: CEN5038 NP

CURRENT APPLICATION NUMBER: US/10/953,613C

PRIOR FILING DATE: 2004-09-29

PRIOR APPLICATION NUMBER: 60/507,231

NUMBER OF SEQ ID NOS: 1021

SOFTWARE: PatentIn Ver 3.0

SEQ ID NO 780

LENGTH: 12

TYPE: PRT

ORGANISM: Homo sapiens

US-10-953-613C-780

Query Match 58.1%; Score 61; DB 6; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.003;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 QETFSDLWKLLP 16  
| | | | | | | | | | | | | |  
Db 1 QETFSDLWKLLP 12

RESULT 4  
US-10-953-613C-792

Sequence 792, Application US/10953613C  
Publication No. US20060127404A1

GENERAL INFORMATION:

APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallan;  
APPLICANT: Bernard;Nesspor; Thomas

TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES

FILE REFERENCE: CEN5038 NP

CURRENT APPLICATION NUMBER: US/10/953,613C

PRIOR FILING DATE: 2004-09-29

PRIOR APPLICATION NUMBER: 60/507,231

NUMBER OF SEQ ID NOS: 1021

SOFTWARE: PatentIn Ver 3.0

SEQ ID NO 792

LENGTH: 12

TYPE: PRT

ORGANISM: Homo sapiens

US-10-953-613C-792

Query Match 58.1%; Score 61; DB 6; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.003;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 QETFSDLWKLLP 16  
| | | | | | | | | | | | | |  
Db 1 QETFSDLWKLLP 12

RESULT 5

US-10-953-613C-779

Sequence 779, Application US/10953613C  
Publication No. US20060127404A1

GENERAL INFORMATION:

APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallan;  
APPLICANT: Bernard;Nesspor; Thomas

TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES

FILE REFERENCE: CEN5038 NP

CURRENT APPLICATION NUMBER: US/10/953,613C

CURRENT FILING DATE: 2004-09-29

PRIOR APPLICATION NUMBER: 60/507,231

PRIOR FILING DATE: 2003-09-30

NUMBER OF SEQ ID NOS: 1021

SOFTWARE: PatentIn Ver 3.0

SEQ ID NO 779

LENGTH: 12

TYPE: PRT

ORGANISM: Homo sapiens

US-10-953-613C-779

Query Match 57.1%; Score 60; DB 6; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.0042;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 QETFSDLWKLLP 16  
| | | | | | | | | | | | | |  
Db 1 QETFSDLWKLLP 12

RESULT 6  
US-10-953-613C-791

Sequence 791, Application US/10953613C  
Publication No. US20060127404A1

GENERAL INFORMATION:

APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallan;  
APPLICANT: Bernard;Nesspor; Thomas

TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES

FILE REFERENCE: CEN5038 NP

CURRENT APPLICATION NUMBER: US/10/953,613C

CURRENT FILING DATE: 2004-09-29

PRIOR APPLICATION NUMBER: 60/507,231

PRIOR FILING DATE: 2003-09-30

NUMBER OF SEQ ID NOS: 1021

SOFTWARE: PatentIn Ver 3.0

SEQ ID NO 791

LENGTH: 12

TYPE: PRT

ORGANISM: Homo sapiens

US-10-953-613C-791

Query Match 57.1%; Score 60; DB 6; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.0042;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 QETFSDLWKLLP 16  
| | | | | | | | | | | | | |  
Db 1 QETFSDLWKLLP 12

RESULT 7  
US-10-538-066-624

Sequence 624, Application US/10538066  
Publication No. US20060094649A1

GENERAL INFORMATION:

APPLICANT: BpImmune Inc.

TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen

FILE REFERENCE: 2060.015PC06

CURRENT APPLICATION NUMBER: US/10/538,066

CURRENT FILING DATE: 2005-06-09

PRIOR APPLICATION NUMBER: US 60/432,017

PRIOR FILING DATE: 2002-12-10

NUMBER OF SEQ ID NOS: 767

```

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 624
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-624
```

```

Query Match          56.2%; Score 59; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY      5 QETFSDLWKLL 15
        |||||
Db      1 QETFSDLWKLL 11
```

```

RESULT 8
US-10-538-066-600
; Sequence 600, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
```

```

; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 600
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-600
```

```

Query Match          52.4%; Score 55; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      5 QETFSDLWKLL 14
        |||||
Db      1 QETFSDLWKLL 10
```

```

RESULT 9
US-10-953-613C-781
; Sequence 781, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallion;
; APPLICANT: Bernard;Nespor; Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 781
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-781
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```

Query Match          52.4%; Score 55; DB 6; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      5 QETFSDLWKLLP 16
        |||||
```

```

Db      1 QETFSDWKLLP 12
```

```

RESULT 10
US-10-953-613C-793
; Sequence 793, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
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```

; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallion;
; APPLICANT: Bernard;Nespor; Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 793
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-793
```

```

Query Match          52.4%; Score 55; DB 6; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      5 QETFSDLWKLLP 16
        |||||
Db      1 QETFSDWKLLP 12
```

```

RESULT 11
US-10-538-066-353
; Sequence 353, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
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; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 353
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-353
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Query Match          46.7%; Score 49; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY      7 TFSDLWKLL 15
        |||||
Db      1 TFSDLWKLL 9
```

```

RESULT 12
US-10-538-066-623
; Sequence 623, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
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; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
```

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; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 623
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-623
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Query Match
Best Local Similarity 41.0%; Score 43; DB 6; Length 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 PPLSOETF 8
Db 3 PPLSOETF 10
```

```
RESULT 13
US-10-538-066-354
; Sequence 354, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
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; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 354
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-354
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```
Query Match
Best Local Similarity 40.0%; Score 42; DB 6; Length 9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 7 TFSIDLWKL 14
Db 1 TFSIDLWKL 8
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```
RESULT 14
US-10-538-066-622
; Sequence 622, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
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APPLICANT: Epimmune Inc.  
TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen  
FILE REFERENCE: 2060.015PC06  
CURRENT APPLICATION NUMBER: US/10/538,066  
CURRENT FILING DATE: 2005-06-09  
PRIOR APPLICATION NUMBER: US 60/432,017  
PRIOR FILING DATE: 2002-12-10  
NUMBER OF SEQ ID NOS: 767  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 622  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-538-066-622

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Query Match
Best Local Similarity 35.2%; Score 37; DB 6; Length 9;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 PPLSOETF 7
Db 3 PPLSOETF 9
```

```
RESULT 15
US-10-953-613C-777
; Sequence 777, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
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APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Chravetb, John;Scallion;  
TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES  
FILE REFERENCE: CEN5038 NP  
CURRENT APPLICATION NUMBER: US/10/953,613C  
CURRENT FILING DATE: 2004-09-29  
PRIOR APPLICATION NUMBER: 60/507,231  
PRIOR FILING DATE: 2003-09-30  
NUMBER OF SEQ ID NOS: 1021  
SOFTWARE: PatentIn Ver 3.0  
SEQ ID NO 777  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-953-613C-777

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Query Match
Best Local Similarity 34.3%; Score 36; DB 6; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 7 TFSIDLW 12
Db 1 TFSIDLW 6
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Search completed: July 5, 2006, 23:04:32
Job time : 22 secs
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2006, 22:59:36 ; Search time 50 Seconds  
(without alignments)  
33.262 Million cell updates/sec

Title: US-09-403-440A-2  
Perfect score: 105  
Sequence: 1 PLSQETFSIDMKLPLENG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 276470

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	92	87.6	19	2	US-09-732-384-7	Sequence 7, Appl1
2	90	85.7	19	2	US-09-081-975-13	Sequence 13, Appl1
3	81	77.1	15	2	US-09-581-472B-4	Sequence 4, Appl1
4	77	73.3	15	1	US-08-277-660A-1	Sequence 1, Appl1
5	77	73.3	15	1	US-08-277-660A-4	Sequence 4, Appl1
6	77	73.3	15	1	US-08-424-957-1	Sequence 1, Appl1
7	77	73.3	15	1	US-08-424-957-20	Sequence 20, Appl1
8	77	73.3	15	2	US-09-035-686-1	Sequence 1, Appl1
9	77	73.3	15	2	US-09-035-686-20	Sequence 20, Appl1
10	77	73.3	15	2	US-09-732-384-6	Sequence 6, Appl1
11	74	70.5	15	1	US-08-277-660A-5	Sequence 5, Appl1
12	74	70.5	15	1	US-08-424-957-21	Sequence 21, Appl1
13	74	70.5	15	2	US-09-035-686-21	Sequence 21, Appl1
14	74	70.5	16	2	US-09-081-975-23	Sequence 23, Appl1
15	74	70.5	18	2	US-09-695-437A-63	Sequence 63, Appl1
16	73	69.5	15	2	US-09-695-437A-8	Sequence 8, Appl1
17	70	66.7	13	2	US-09-695-437A-42	Sequence 42, Appl1
18	70	66.7	13	2	US-09-701-080C-22	Sequence 22, Appl1
19	70	66.7	13	2	US-09-701-080C-27	Sequence 27, Appl1
20	70	66.7	15	2	US-09-695-437A-22	Sequence 22, Appl1
21	69	65.7	17	2	US-09-695-437A-40	Sequence 40, Appl1
22	66	62.9	12	2	US-09-428-082B-131	Sequence 131, Appl1
23	66	62.9	12	2	US-09-428-082B-143	Sequence 143, Appl1
24	66	62.9	18	2	US-09-695-437A-64	Sequence 64, Appl1
25	65	61.9	15	2	US-09-280-047-6	Sequence 6, Appl1
26	65	61.9	15	2	US-08-208-573B-6	Sequence 6, Appl1

27	65	61.9	15	2	US-09-258-981-3	Sequence 3, App1
28	65	61.9	15	2	US-09-511-204B-3	Sequence 3, App1
29	65	61.9	15	2	US-09-950-692-6	Sequence 6, App1
30	65	61.9	15	2	US-09-695-437A-11	Sequence 11, App1
31	65	61.9	15	5	PCT-US95-02856-6	Sequence 6, App1
32	62	59.0	15	2	US-09-695-437A-16	Sequence 16, App1
33	62	59.0	15	2	US-09-695-437A-21	Sequence 21, App1
34	62	59.0	15	2	US-09-695-437A-32	Sequence 32, App1
35	61	58.1	12	2	US-09-428-082B-133	Sequence 133, App
36	61	58.1	12	2	US-09-428-082B-145	Sequence 145, App
37	61	58.1	15	2	US-09-695-437A-13	Sequence 13, App1
38	60	57.1	12	2	US-09-428-082B-132	Sequence 132, App
39	60	57.1	12	2	US-09-428-082B-144	Sequence 144, App
40	60	57.1	15	2	US-09-695-437A-33	Sequence 33, App1
41	60	57.1	18	2	US-09-081-975-22	Sequence 22, App1
42	59	56.2	11	1	US-08-277-660A-9	Sequence 9, App1
43	59	56.2	11	1	US-08-424-957-17	Sequence 17, App1
44	59	56.2	11	2	US-09-035-686-17	Sequence 17, App1
45	59	56.2	11	2	US-09-603-052-5	Sequence 5, App1

## ALIGNMENTS

```
RESULT 1
US-09-732-384-7
; Sequence 7, Application US/09732384
; Patent No. 6831155
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Protein
; OTHER INFORMATION: Fragment not in inhibitory p53 polypeptide
US-09-732-384-7

Query Match      87.6%; Score 92; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PLSQETFSIDMKLPLEN 18
Db      1 PLSQETFSIDMKLPLEN 17

RESULT 2
US-09-081-975-13
; Sequence 13, Application US/09081975
; Patent No. 6451979
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
```

COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,975  
FILING DATE: 12-MAY-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/046,207  
FILING DATE: 12-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-081-975-13

Query Match 85.7%; Score 90; DB 2; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1,1e-07;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDDLWKLPEN 18  
|||||:|||||  
Db 1 PPLSQETFSDDLWKLPEN 18

RESULT 3  
US-09-581-472B-4  
Sequence 4, Application US/09581472B  
Patent No. 6818744  
GENERAL INFORMATION:  
APPLICANT: FRADY, Raymond  
TITLE OF INVENTION: P53 REGULATORY PROTEIN CALLED RB18A AND USES THEREOF  
FILE REFERENCE: P06781US00/BAS  
CURRENT APPLICATION NUMBER: US/09/581,472B  
CURRENT FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: PCT/EP96/08560  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: EP 97403051.2  
PRIOR FILING DATE: 1997-12-15  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: The artificial sequence is a nucleic acid.  
US-09-581-472B-4

Query Match 77.1%; Score 81; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2,3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLSQETFSDDLWKLP 16  
|||||:|||||  
Db 1 PLSQETFSDDLWKLP 15

RESULT 4

US-08-277-660A-1  
Sequence 1, Application US/08277660A  
Patent No. 5702908  
GENERAL INFORMATION:  
APPLICANT: Picklesley, Steven M.  
TITLE OF INVENTION: Interruption of Binding of MDK2 and P53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/277,660A  
FILING DATE: 20-JUL-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-60244/WHI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-277-660A-1

Query Match 73.3%; Score 77; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDDLWKLPEN 18  
|||||:|||||  
Db 1 QETFSDDLWKLPEN 14

RESULT 5  
US-08-277-660A-4  
Sequence 4, Application US/08277660A  
Patent No. 5702908  
GENERAL INFORMATION:  
APPLICANT: Picklesley, Steven M.  
TITLE OF INVENTION: Interruption of Binding of MDK2 and P53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/277,660A  
FILING DATE: 20-JUL-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Dieger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-60244/WHD  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-277-660A-4

Query Match 73.3%; Score 77; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQTFSDLWKL 14  
Db 2 PPLSQTFSDLWKL 15

RESULT 6  
US-08-424-957-1  
Sequence 1, Application US/08424957  
Patent No. 5770377  
GENERAL INFORMATION:  
APPLICANT: Picksley, Steven M.  
APPLICANT: Lane, David P.  
TITLE OF INVENTION: Interruption of Binding of MDM2 and p53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fleht, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,957  
FILING DATE: 19-APR-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,660  
FILING DATE: 20-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dieger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-61228/WHD  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
US-08-424-957-1

Query Match 73.3%; Score 77; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 QETFSDLWKLLEN 18  
Db 1 QETFSDLWKLLEN 14

RESULT 7  
US-08-424-957-20  
Sequence 20, Application US/08424957  
Patent No. 5770377  
GENERAL INFORMATION:  
APPLICANT: Picksley, Steven M.  
APPLICANT: Lane, David P.  
TITLE OF INVENTION: Interruption of Binding of MDM2 and p53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fleht, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,957  
FILING DATE: 19-APR-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,660  
FILING DATE: 20-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dieger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-61228/WHD  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
US-08-424-957-20

Query Match 73.3%; Score 77; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQTFSDLWKL 14  
Db 2 PPLSQTFSDLWKL 15

RESULT 8  
US-09-035-686-1  
Sequence 1, Application US/09035666  
Patent No. 6153391  
GENERAL INFORMATION:  
APPLICANT: Picksley, Steven M.  
APPLICANT: Lane, David P.  
TITLE OF INVENTION: Interruption of Binding of MDM2 and p53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 50

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-09-035-686-1

Query Match          73.3%; Score 77; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QETFSDLWKLPEN 18
        |||||
Db      1 QETFSDLWKLPEN 14

RESULT 9
US-09-035-686-20
; Sequence 20, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Picklesley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDW2 and p53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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```
;
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-09-035-686-20

Query Match          73.3%; Score 77; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PPLSQETFSDLWKL 14
        |||||
Db      2 PPLSQETFSDLWKL 15

RESULT 10
US-09-732-384-6
; Sequence 6, Application US/09732384
; Patent No. 6831155
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Protein
; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
;
US-09-732-384-6

Query Match          73.3%; Score 77; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QETFSDLWKLPEN 18
        |||||
Db      1 QETFSDLWKLPEN 14

RESULT 11
US-08-277-660A-5
; Sequence 5, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Picklesley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDW2 and p53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/277,660A  
FILING DATE: 20-JUL-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE//DOCKET NUMBER: A-60244/MHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-277-660A-5

Query Match 70.5%; Score 74; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 3e-05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLLP 16  
Db 1 PLSQETFSGLMKLLP 15

RESULT 12  
US-08-424-957-21  
Sequence 21, Application US/08424957  
Patent No. 5770377  
GENERAL INFORMATION:  
APPLICANT: Picksley, Steven M.  
TITLE OF INVENTION: Interruption of Binding of MDM2 and p53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,957  
FILING DATE: 19-APR-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,660  
FILING DATE: 20-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE//DOCKET NUMBER: A-61228/MHD

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
US-08-424-957-21

Query Match 70.5%; Score 74; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 3e-05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLLP 16  
Db 1 PLSQETFSGLMKLLP 15

RESULT 13  
US-09-035-686-21  
Sequence 21, Application US/09035686  
Patent No. 6153391  
GENERAL INFORMATION:  
APPLICANT: Picksley, Steven M.  
TITLE OF INVENTION: Interruption of Binding of MDM2 and p53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/035,686  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/424,957  
FILING DATE: 19-APR-1995  
APPLICATION NUMBER: US 08/277,660  
FILING DATE: 20-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE//DOCKET NUMBER: A-61228/MHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
US-09-035-686-21

Query Match 70.5%; Score 74; DB 2; Length 15;  
Best Local Similarity 93.3%; Pred. No. 3e-05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLLP 16

Db 1 PLSQETFSGLWKLLP 15

```
RESULT 14
US-09-081-975-23
; Sequence 23, Application US/09081975
; Patent No. 6451979
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-081-975-23

Query Match 70.5%; Score 74; DB 2; Length 16;
Best Local Similarity 81.2%; Pred. No. 3.2e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PLSQETFSGLWKLLP 17
Db 1 PLSQETFSGLWKLLP 16

RESULT 15
US-09-695-437A-63
; Sequence 63, Application US/09695437A
; Patent No. 6803203
; GENERAL INFORMATION:
; APPLICANT: Brookhaven Science Associates
; APPLICANT: Anderson, Carl W
; APPLICANT: Connolly, Margery A
; TITLE OF INVENTION: DNA-PK Assay
; FILE REFERENCE: BSA 01-02
; CURRENT APPLICATION NUMBER: US/09/695,437A
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/398,139
; PRIOR FILING DATE: 1995-03-03
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; PRIOR APPLICATION NUMBER: 08/132,284
; PRIOR FILING DATE: 1993-10-06
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: DNA-PK synthetic substrate based on human p53 residues 14-28
US-09-695-437A-63
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Query Match 70.5%; Score 74; DB 2; Length 18;
Best Local Similarity 93.3%; Pred. No. 3.7e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLSQETFSGLWKLLP 16
Db 1 PLSQETFSGLWKLLP 15
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Search completed: July 5, 2006, 23:00:59  
Job time : 51 secs